

Publication No. US20030104482A1
GENERAL INFORMATION:
APPLICANT: Immunex Corp.
APPLICANT: Bird, Timothy
APPLICANT: Vitea, G.D.
TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS
FILE OF INVENTION: (DAKAR)
FILE REFERENCE: 2889-US
CURRENT APPLICATION NUMBER: US/10/299,327
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US/09/509,802
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patent version 3.0
SEQ ID NO 2
LENGTH: 786
TYPE: PRT
ORGANISM: Mus sp.
US-10-299-327-2

Query Match 8.3%; Score 302; DB 14; Length 786;
Best Local Similarity 31.0%; Pred. No. 3.9e-18;

Matches 95; Conservative 51; Mismatches 140; Indels 20; Gaps 9;

QY 112 DLIRNPSVVAHLAVELGIRCFHHSRIISCANCAENEGCTPLHLAC-RKGDGEIIVE 170
DB 434 DLVLD-SSASLHLAVEAQGECEVKMLLNANPNLTNRKGSTPLHMAVERKRG--IVE 490
QY 171 LVQYCHTQMDVDYKGETVFFHYAVQ-GDNSQVQLQIGRNAVAGLNOVNOGLTPLHLAQ 229
DB 491 LILARTSVNADEQDWTALHFAQNGDEASTRLLEKN--ASVNEVDEGRTPMHIVACQ 548
QY 230 LKQEMVRVLLCNARCINMGNGY-PIHSAMFSGKCAEMISDSQHSKDPRYGA 288
DB 549 HGOENIVRTLRRGVAVGQGDAMLPHYAMQGHLPVKKLAQPGVSVNAQ-TLDR 607
QY 289 SPLHMAK--NAEMARMLKRCGNVSTSSAGNTALHGVMBRRPDCATVLLTHGANADA 345
DB 608 TPLHLAQAQGHYVARILIDCSQVNICSLQAOPTPLHVALETGHTSTALLHHRGAKXA 667
QY 346 RGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTPNDFGETPTFLASKIGKIQ----- 397
DB 668 LTSEGYTALHLAQAQNGHLATVLLIEKADVMARGPLNQTALHLAARGHSEVEBELVGA 727
QY 398 DLMHIS 403
DB 728 DLIIDS 733

RESULT 14
US-10-128-174-13

Sequence 13, Application US/10128174
Publication No. US20030199462A1
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/10/128,174
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patent version 3.1
SEQ ID NO 13
LENGTH: 786
TYPE: PRT
ORGANISM: Mus musculus
US-10-128-174-13

Query Match 8.3%; Score 302; DB 14; Length 786;
Best Local Similarity 31.0%; Pred. No. 3.9e-18;

Matches 95; Conservative 51; Mismatches 140; Indels 20; Gaps 9;

QY 112 DLIRNPSVVAHLAVELGIRCFHHSRIISCANCAENEGCTPLHLAC-RKGDGEIIVE 170

DB 434 DLVLD-SSASLHLAVEAQGECEVKMLLNANPNLTNRKGSTPLHMAVERKRG--IVE 490
QY 171 LVQYCHTQMDVDYKGETVFFHYAVQ-GDNSQVQLQIGRNAVAGLNOVNOGLTPLHLAQ 229
DB 491 LILARTSVNADEQDWTALHFAQNGDEASTRLLEKN--ASVNEVDEGRTPMHIVACQ 548
QY 230 LKQEMVRVLLCNARCINMGNGY-PIHSAMFSGKCAEMISDSQHSKDPRYGA 288
DB 549 HGOENIVRTLRRGVAVGQGDAMLPHYAMQGHLPVKKLAQPGVSVNAQ-TLDR 607
QY 289 SPLHMAK--NAEMARMLKRCGNVSTSSAGNTALHGVMBRRPDCATVLLTHGANADA 345
DB 608 TPLHLAQAQGHYVARILIDCSQVNICSLQAOPTPLHVALETGHTSTALLHHRGAKXA 667
QY 346 RGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTPNDFGETPTFLASKIGKIQ----- 397
DB 668 LTSEGYTALHLAQAQNGHLATVLLIEKADVMARGPLNQTALHLAARGHSEVEBELVGA 727
QY 398 DLMHIS 403
DB 728 DLIIDS 733

RESULT 15
US-10-128-174-31

Sequence 31, Application US/10128174
Publication No. US20030199462A1
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/10/128,174
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patent version 3.1
SEQ ID NO 31
LENGTH: 786
TYPE: PRT
ORGANISM: Mus musculus
US-10-128-174-31

Query Match 8.3%; Score 302; DB 14; Length 786;
Best Local Similarity 31.0%; Pred. No. 3.9e-18;

Matches 95; Conservative 51; Mismatches 140; Indels 20; Gaps 9;

QY 112 DLIRNPSVVAHLAVELGIRCFHHSRIISCANCAENEGCTPLHLAC-RKGDGEIIVE 170
DB 434 DLVLD-SSASLHLAVEAQGECEVKMLLNANPNLTNRKGSTPLHMAVERKRG--IVE 490
QY 171 LVQYCHTQMDVDYKGETVFFHYAVQ-GDNSQVQLQIGRNAVAGLNOVNOGLTPLHLAQ 229
DB 491 LILARTSVNADEQDWTALHFAQNGDEASTRLLEKN--ASVNEVDEGRTPMHIVACQ 548
QY 230 LKQEMVRVLLCNARCINMGNGY-PIHSAMFSGKCAEMISDSQHSKDPRYGA 288
DB 549 HGOENIVRTLRRGVAVGQGDAMLPHYAMQGHLPVKKLAQPGVSVNAQ-TLDR 607
QY 289 SPLHMAK--NAEMARMLKRCGNVSTSSAGNTALHGVMBRRPDCATVLLTHGANADA 345
DB 608 TPLHLAQAQGHYVARILIDCSQVNICSLQAOPTPLHVALETGHTSTALLHHRGAKXA 667
QY 346 RGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTPNDFGETPTFLASKIGKIQ----- 397
DB 668 LTSEGYTALHLAQAQNGHLATVLLIEKADVMARGPLNQTALHLAARGHSEVEBELVGA 727
QY 398 DLMHIS 403
DB 728 DLIIDS 733

Search completed: May 26, 2005, 14:51:06

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; TYPE: PR1
; ORGANISM: Caenorhabditis elegans
US-10-369-493-4998

Query Match
Best Local Similarity 27.0%; Score 324.5; DB 15; Length 468;
Matches 110; Conservative 74; Mismatches 164; Indels 59; Gaps 16;

QY 286 YGASPLHMAKNAMARMLKRGCVNVSTSSAGNTALHVGVRN----RFDCAIVLITTHG 340
DB 44 YDLSTVITWLN--LRFLLISRYCR-----SENVCHNLBALMNAARYGNTDLTKLYITH 94

QY 341 AAMDAGEHNTPLHLSKDNVEMIKALIVFGAEVD---TPNDFGTPPLASKIGKIQ 397
DB 95 IDLRMTDETGTMTAHVAVMNQKIVMLVYLCAPCQIMKIKNNNGLTSTELCTDKKISE 154

QY 398 DLMHISRRARKE--AF-----LIGSRDEKRTHDH-LLCIDGGGVGLITITOLLA 444
DB 155 DFRSLNPNPSPSGAIFVDVNSEYNNVILASERKQWKEPERVLLADGGGIRAIVITIQMLH 214

QY 445 IERKASGVATKDLPEWVAGTSTGGILALAI-LHSKSMAYMRGMYFRMKDEYF-RGSR---P 499
DB 215 IDYLLGGLVEKLDIAGTSCGGVITLLSTNNRNIEETRKLLDMDRDFITGADKAVP 274

QY 500 YESGPLEEPFKRPF--GEHTKRTDVKKPKYMLTGTLSDRQPAELHFRNT--DAPEYRE 555
DB 275 KYSSNGMEYIARVYTTWEDSKMSIKRHRALIVVADTRMVPOLLFRSYRPEWPEACE 334

QY 556 P-RFNQNVMLRPPAPSDQLWMPAASSGAAPTYFRPNRGRFLDGGGLANNPTLDAMTEIH 614
DB 335 HYKF-----LDPTKVELMKTLCRTTAAPIFFESFNSLSDGGLANNPTLALISDF 385

QY 615 EYNQDLIRKQANKV-----KLSIVSLGTGRSPQVPVTCVDV 653
DB 386 LFKK-LKESFAKSSSERENRGNMKIGCVISLGTGVPEFKIGIDIL 430

RESULT 11
US-10-108-260A-3237
; Sequence 3237, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3237
; LENGTH: 1330
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-108-260A-3237

Query Match
Best Local Similarity 27.0%; Score 324; DB 15; Length 1330;
Matches 99; Conservative 62; Mismatches 128; Indels 77; Gaps 9;

QY 103 HTEVLOHLD-----LIRNHPMSVAHLAVELGIRGCFHH-----SRIT 141
DB 290 HDQVVELLERGAPLARTKNGSLPLMAAQGDHVECVKHLQHKAEVDDVTLDYLTALH 349

QY 142 SCANC-----AENEGCTPLHACRGKGDGELLVLEVOY----- 174
DB 350 VAACHGHYRTKLLDKRANPNARALNGFTPLHACKKRIKWELLVYKIGASIQAITES 409

QY 175 ----CH-----TQMDVTDYKGETVFHYAVQDSQVQLLGRNAVAG 212
DB 410 GLTPHVAAFMGHLNITVILLQNGASPDVTNINGETALHMAAARGVEVVRCLLRNG-AL 468

QY 213 LNOVNNQGLTPLHLACQLGQENYRVULLCNARCINIGPNGY-PHSAMKFSQKCAEMI 271
DB 213 LNOVNNQGLTPLHLACQLGQENYRVULLCNARCINIGPNGY-PHSAMKFSQKCAEMI 271
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DB 469 VDAAREEQTPHLIARLKTETIVOLLQHMHPDAATTNRYTPHLHSAREQGVDAVSL 528
QY 272 ISMDSQIHSKDBDRYASPLHMAK--NEMAMRLKRGCVNVSTSSAGNTALHVGVRN 328
DB 529 --LEAGASLATAKSGFTPLHVAKYGSLDVAKLLQRRADAASAGNGLTPHVAHYD 586
QY 329 RFDCAIVLTHGANNAARGHNTPLHLSKDNVEMIKALIVFGAEVDTPNDFGTPPLF 388
DB 587 NQRYALLLEKSGSPHATKNGYTPHLIAKKNQKQOIASTLLNVAERTNIVTYQGVTPH 646

QY 389 LASKIG 394
DB 647 LASQEG 652

RESULT 12
US-10-164-080-2
; Sequence 2, Application US/10164080
; Publication No. US20030087411A1
; GENERAL INFORMATION:
; APPLICANT: BIRD, Timothy, A.
; APPLICANT: HOLLAND, Pamela, M.
; APPLICANT: PESCHON, Jacques, J.
; APPLICANT: VIRCA, George, D.
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS (DAKAR) AND ME1
; FILE REFERENCE: 3280-B
; CURRENT APPLICATION NUMBER: US/10/164,080
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/295,959
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/334,362
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 786
; TYPE: PR1
; ORGANISM: Mus sp.
US-10-164-080-2

Query Match
Best Local Similarity 31.0%; Score 302; DB 14; Length 786;
Matches 95; Conservative 51; Mismatches 140; Indels 20; Gaps 9;

QY 112 DLIRNHPMSVAHLAVELGIRGCFHHSRIITSCANCAENEGCTPLHAC-RKGDGETIVE 170
DB 434 DLYLD-SSASLHLAYEAGQEECVKMLLNANPNLITNRKGSTPLHMAVERKRG--IVE 430

QY 171 LVQYCHTQMDVTDYKGETVFHYAVQ--GDSQVQLQLLGRNAVAGLNQVNNQGLTPLHLACQ 229
DB 491 LILARTSVNAKQEDQWTLAHFAQNGDEASTRLLEKN--ASVNEVDFFGRTPMHVAQ 548

QY 230 LKQENYRVULLCNARCINIGPNGY-PHSAMKFSQKCAEMIISMDSQIHSKDBRYGA 288
DB 549 HGGENTIVTRLIRGVDVNGLOGKDAMLPRLHYAAMQGHLPYKLAKQPGVSVNQ-FLDGR 607

QY 289 SPLHMAK--NEMAMRLKRGCVNVSTSSAGNTALHVGVRNRPFCALIVLTHGANADA 345
DB 608 TPLHLLAQRGHYVVAAILLIDLSQVNICSLQAGTPLHVAATGHTSTARLLHRRGAKKEA 667

QY 346 RGEHNTPLHLSKDNVEMIKALIVFGAEVDTPNDFGTEPPLASKIGKIQ----- 397
DB 668 LITSEGYTALHLAQNQHILATVTKLLIEBKADVMAARGPLNQTALHLAARHSEVVEELVSA 727

QY 398 DLMHIS 403
DB 728 DLIIDS 733

RESULT 13
US-10-299-327-2
; Sequence 2, Application US/10299327
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QY 149 NEEGCTPLHLACRKGDEILVELVOYCHTQMDVTYKGETVFHYAVQDNGSVOLLL--G 206
DB 316 QPEGSLPMTIAVQNTQIEVSWMLDH--GADNITLISSEGQNVLAHVAATASSGDLIKILMET 374
QY 207 RNAVAGLNQVNOGLTPLHLACQLGKQKQEMVRVLLCNARCNITMGPNG-----Y 254
DB 375 KKECFMINQTDNSNGTTPAVVA-----LINCLSNCOQLRGRGGIIGSSDSTOMAN 424
QY 255 PIHSAMKFSQ--KGAEMTISDSSQIHSKDPRYGASPLHMAKNAEMAMMLKR---GCN 309
DB 425 PIIGAMKRGKLDVSLRKLKELKODGLTETEPPTGNVTVHCAINKKCLILMEKRDQTD 484
QY 310 VNSTSSAGNTALHVGVMNRFPDCAIVLLTHGANADARGHNTPLHLAMSKDNVEMIKAL 369
DB 485 PEARNALQOTPLHTFVILDEGLVMTLSAYGVMDPAQDINGNTPLHCAVTRGNTIARML 544
QY 370 IVFGAEVDTPNDFGPTPLFASKIGKLODLMHISBAR-----KPAFI----- 411
DB 545 ICLGAKPDIKNRKYKSPHIAARLTKERAKMDIVRALIICGAGACDDGFIGCAFQGMHKT 604
QY 412 -----LGSN-----RDEKRT 421
DB 605 GLTSCKTQIGSSSSDEQSMEDRVKDIHVSNAASAPYEFVLDPDTQLVEAAYERNETRA 664
QY 422 HDH-----LCLDGGVGKGLIITOLLIAIEKASGVATKOL 456
DB 665 FPEBALRKVRNKKLKEVKKTSNVINVLGDDGIRGLVTVQMLICAEALDRPLIDY 724
QY 457 FDMVAGTSTGILALAIHSHSKMAYRMGYFFMKQEVFRG--SRPESGPLEEFLKREFGE 515
DB 725 FWMIGATSTGCIYIMSTMWMTGSLRKAQRYLWFKQDLFDSWTRPVDTKLLEFIQAFGA 784
QY 516 HTRMTDVRKPKWMLTGLSDRQPAELHFRNYDAETVAREPFRNONVNLPPAOPSQOLV 575
DB 785 DRLMDIKYRPFECTTVADTFPVQLELRNRLPISKE---NNDLGF---TDPELTI 838
QY 576 WRAARSSGAAPTYFRPN--GRFLDGLANPTLDANTEIHEYNOULIRKQANKVKLSI 634
DB 839 WATRRSSAAPTFFSASEGKFDGGMISNPPVLDMSDIGFNTTCCQKRIPEKAVDMGC 898
QY 635 VVSLGTGRSPQVPVTCVDFRPSNPWELAKTVFGAKELGKMYVDDCTDDBGRP 687
DB 899 VLSVGTGITPICVD--PSVFEMNDLFGMLR---GKNLSLVVIDQATATEGAP 947

RESULT 9
US-10-369-493-6690
; Sequence 6690, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6690
; LENGTH: 1023
; TYPE: PR1
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6690

Query Match 17.5%; Score 634.5; DB 15; Length 1023;
Best Local Similarity 24.2%; Pred. No. 1,8e-48;
Matches 187; Conservative 148; Mismatches 287; Indels 151; Gaps 21;

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QY 37 RYREBQULILFQNTENRNTWDCVLNPNRSOGGFRLLFOLEAD--ALVNFHOYSQQLPF 94
DB 204 RAKEEEL---KNKRLYLALITLVNENNEKYMSLFRSHKLADVALCERCENPELFRV 260
QY 95 YESSPOV---LHTEVLOHLTDLIRNHPGMSVAHLAVEIGIRCEFH---SRILISCANCAE 148
DB 261 FPKXVNIKDYLIHT-----IFHELRLDNMTWKSVAHSSKIGLETFEYFENMEKHKKIKYINTLV 315
QY 149 NEEGCTPLHLACRKGDEILVELVOYCHTQMDVTYKGETVFHYAVQDNGSVOLLL--G 206
DB 316 QPEGSLPMTIAVQNTQIEVSWMLDH--GADNITLISSEGQNVLAHVAATASSGDLIKILMET 374
QY 207 RNAVAGLNQVNOGLTPLHLACQLGKQKQEMVRVLLCNARCNITMGPNG-----Y 254
DB 375 KKECFMINQTDNSNGTTPAVVA-----LINCLSNCOQLRGRGGIIGSSDSTOMAN 424
QY 255 PIHSAMKFSQ--KGAEMTISDSSQIHSKDPRYGASPLHMAKNAEMAMMLKR---GCN 309
DB 425 PIIGAMKRGKLDVSLRKLKELKODGLTETEPPTGNVTVHCAINKKCLILMEKRDQTD 484
QY 310 VNSTSSAGNTALHVGVMNRFPDCAIVLLTHGANADARGHNTPLHLAMSKDNVEMIKAL 369
DB 485 PEARNALQOTPLHTFVILDEGLVMTLSAYGVMDPAQDINGNTPLHCAVTRGNTIARML 544
QY 370 IVFGAEVDTPNDFGPTPLFASKIGKLODLMHISBAR-----KPAFI----- 411
DB 545 ICLGAKPDIKNRKYKSPHIAARLTKERAKMDIVRALIICGAGACDDGFIGCAFQGMHKT 604
QY 412 -----LGSN-----RDEKRT 421
DB 605 GLTSCKTQIGSSSSDEQSMEDRVKDIHVSNAASAPYEFVLDPDTQLVEAAYERNETRA 664
QY 422 HDH-----LCLDGGVGKGLIITOLLIAIEKASGVATKOL 456
DB 665 FPEBALRKVRNKKLKEVKKTSNVINVLGDDGIRGLVTVQMLICAEALDRPLIDY 724
QY 457 FDMVAGTSTGILALAIHSHSKMAYRMGYFFMKQEVFRG--SRPESGPLEEFLKREFGE 515
DB 725 FWMIGATSTGCIYIMSTMWMTGSLRKAQRYLWFKQDLFDSWTRPVDTKLLEFIQAFGA 784
QY 516 HTRMTDVRKPKWMLTGLSDRQPAELHFRNYDAETVAREPFRNONVNLPPAOPSQOLV 575
DB 785 DRLMDIKYRPFECTTVADTFPVQLELRNRLPISKE---NNDLGF---TDPELTI 838
QY 576 WRAARSSGAAPTYFRPN--GRFLDGLANPTLDANTEIHEYNOULIRKQANKVKLSI 634
DB 839 WATRRSSAAPTFFSASEGKFDGGMISNPPVLDMSDIGFNTTCCQKRIPEKAVDMGC 898
QY 635 VVSLGTGRSPQVPVTCVDFRPSNPWELAKTVFGAKELGKMYVDDCTDDBGRP 687
DB 899 VLSVGTGITPICVD--PSVFEMNDLFGMLR---GKNLSLVVIDQATATEGAP 947

RESULT 10
US-10-369-493-4998
; Sequence 4998, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4998
; LENGTH: 468

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SEQUENCE CHARACTERISTICS:
 LENGTH: 292 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 US-09-927-180-19

Query Match 42.3%; Score 1531; DB 9; Length 292;
 Best Local Similarity 100.0%; Pred. No. 1.4e-131;
 Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 396 LODLMIHSRRKRAFLIGSMRDEKRTDHLCLDGGVKGKLIITQLIAIEKASGVAIKD 455
DB 1 LODLMIHSRRKRAFLIGSMRDEKRTDHLCLDGGVKGKLIITQLIAIEKASGVAIKD 60
QY 456 LEPDVAAGTSGGILALAILHSKSMAYVRGMYFRMKDEVFGRSRYESGPLEEFLKRFGE 515
DB 61 LEPDVAAGTSGGILALAILHSKSMAYVRGMYFRMKDEVFGRSRYESGPLEEFLKRFGE 120
QY 516 HTKMTDVRKPKWMLTGLSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQPSPDQV 575
DB 121 HTKMTDVRKPKWMLTGLSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQPSPDQV 180
QY 576 WRARSSGAAPTYFRPRGRFLDGGILANPTLDAMTEIHEYNODLIRKQANKVKKLSIV 635
DB 181 WRARSSGAAPTYFRPRGRFLDGGILANPTLDAMTEIHEYNODLIRKQANKVKKLSIV 240
QY 636 VSLGTSRSPQVPVTCVDFPRSPNWEIAKTIVFGAKELGKRVVDCCTDPDGRP 687
DB 241 VSLGTSRSPQVPVTCVDFPRSPNWEIAKTIVFGAKELGKRVVDCCTDPDGRP 292

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RESULT 7
 US-10-369-493-6665
 ; Sequence 6665, Application US/10369493
 ; Publication No. US2003023675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; PRIOR FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 6665
 ; LENGTH: 1071
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 ; US-10-369-493-6665

Query Match 17.9%; Score 647.5; DB 15; Length 1071;
 Best Local Similarity 27.0%; Pred. No. 1.3e-49;
 Matches 194; Conservative 126; Mismatches 260; Indels 139; Gaps 20;

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QY 69 FRLFOLEADALVNFHOYSSQLLPYESSPOVLAITEVL-----QHLTDLIRNHPMSVAH 124
DB 315 FSLFRATDKKDLMDLHLCOEKSFLLTSLDMSMTBADILASKIBELVIGRLRPHYMH 374
QY 125 LAVELEIRCEGTHHSRI-----ISCANCAENBEGCTPLHACKRGDEILVELVOY 174
DB 375 VAIAIDRLDLPFFSGMIKTMMETLEPPESQURCLCHENCYPAHLALTMROKIVERLEL 434
QY 175 CHIQMDVTVYKSGTVHYAVQGNISQVQLLGRNAVAG---LNVANNQGLTPLHLACQLG 221
DB 435 DPTLFCETDKAGNVVHHV---NSSFCAQIIMDRCPASQHFIDBRNMDGQSPINEAVSTA 491

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QY 232 KQEMZVLLLCNARCINMGNGVPIISAMKFSQKCAEMISM-----DSS 277
DB 492 KPLVATFL-----IGKAFPTRGDRNRELFVANTSKNAQSGVEVLTDKP 535
QY 278 QIHSKDPYRGASPLHAKNAEMARMLLKR-----GCNVNSTSSAGNTPLAHGVWRNRPDCA 333
DB 536 EIANERDALGNASIHVALYKESINALLINKRVELGDIIDVGNMNGETRLLLFITTRKDDL 595
QY 334 IVLLT---HGANDARGEHGTPLHLAMS-----KDNVEMIKALIVFGAEVDPNDPGET 385
DB 596 PLIVTLVYAGDANNVATDPHGNTALHKSALVDAKTISLECVKFLISAGSPNKINLRGES 655
QY 386 PTLASKIKGLQDLMIHRA---RKPAFLG-----SMRDE----- 418
DB 656 PRHLAASL-QNOMELAILKAAGATRCPCGYKGRNCRHDCSSAEDEYEETLOKIRIGNE 714
QY 419 -----KRTDHLCLDGGVKGKLIITQLIAIEKASGVA 452
DB 715 SDYEKTEFTASEKLNIDTLDSRRGKAKVNLISMDGGIRGLVLIITQLIAIEBERLGD 774
QY 453 TKDLFPMVAGTSGGILALAILHSKSMAYVRGMYFRMKDEVFGRG-SRPNESGPLEEFLKR 511
DB 775 IFKYPDMSAGTSGSLIMGLATGKSLREMQOTYLLKORVFGIMPEVDTVQLEKFIOD 834
QY 512 EREGHTKMTDVRKPKWMLTGLSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAOPS 571
DB 835 QFQGTGTVWEIPRIMISAVNSEKLPVRLMARANYKPAKDV-----ABETPK 881
QY 572 DQLVRAASSGAAPTYFRPN--GRFLDGGILANPTLDAMTEIHEYNODLIRKQANKVK 630
DB 882 EMLPMALRRSTAPVLFKSEDRYIDGGIISNPALDMSVHAYNRLOLSGRSDAV 941
QY 631 KLSIVSLGTSRSPQVPVTCVDFR--PSNWEIAKTIVFGAKELGKRVVDCCTDPDGRP 687
DB 942 QMNVLVSPFGT---QPSVYIEFLSLIDSNSPLQSIITI---KNLAMPIDQATASGAP 994

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RESULT 8
 US-10-369-493-6689
 ; Sequence 6689, Application US/10369493
 ; Publication No. US2003023675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; PRIOR FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 6689
 ; LENGTH: 1023
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 ; US-10-369-493-6689

Query Match 17.5%; Score 634.5; DB 15; Length 1023;
 Best Local Similarity 24.2%; Pred. No. 1.8e-48;
 Matches 187; Conservative 148; Mismatches 287; Indels 151; Gaps 21;

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QY 37 RVAREGQILIFONTNRTWDCVIVNPRNSQSGRFLFOLELEAD--ALVNFHOYSSQLLP 94
DB 204 RAKEEBEL---KKKPLHYALITLYNNENKRYVMSLFRSHKLADVVALCECRENPELFRV 260
QY 95 YESSPOV---LHTEVQLHLDLIRNHPMSVAHLAVELEIRCEGTHH---SRIISCANCAE 148
DB 261 FPRQNVNIKDYLYHT---IFHELRDMTWKSVHISIKIGLLEFVENMKRHKJLKKYINLTV 315

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Db 102 LCNARCNIMGPNGYPIYSAMKFSQKGCAMTISMDSQIHSKDPYRGASPLHMAKNAEMA 161
Qy 301 RMLLKRGCVNNTSSAGNTALHVGWVRNRPDCAIVLLTHGANADAGEHNTPLHMAK 360
Db 162 RMLLKRGCVNNTSSAGNTALHVGWVRNRPDCAIVLLTHGANADAGEHNTPLHMAK 221
Qy 361 DNVEIMKALIVGAEDVTNDPGEPTPLASKIGK----- 395
Db 222 DNVEIMKALIVGAEDVTNDPGEPTPLASKIGKGLVTRKAILTLRTVGAECPPPIHG 281
Qy 396 -----LQDLMHISPAKPAFLGSMRDEKRTDHL 425
Db 282 VPBAQGAAPHHFSLERAQPPISLNNLELODLMHISPAKPAFLGSMRDEKRTDHL 341
Qy 426 LCLDGGVGVGLIITLIOLIAIEKASGVATKDLFPMVAGTGTGILALAIHSMATWRCM 485
Db 342 LCLDGGVGVGLIITLIOLIAIEKASGVATKDLFPMVAGTGTGILALAIHSMATWRCM 401
Qy 486 YFRMKDEVRGSRPYESGPLEEFLKKEFGENTMTDVRKPKWMLTGLSDROPAELHFR 545
Db 402 YFRMKDEVRGSRPYESGPLEEFLKKEFGENTMTDVRKPKWMLTGLSDROPAELHFR 461
Qy 546 NYDAPETVREPPNQNVLPRPAQPSDQVWRAARSSGAAPTYFRNGRFLDGLLANNP 605
Db 462 NYDAPETVREPPNQNVLPRPAQPSDQVWRAARSSGAAPTYFRNGRFLDGLLANNP 521
Qy 606 TLDAMTEIHEYNODLIRKQANKVKLSIVSLGTRSPQVPTCVDFVRPSNPWELAT 665
Db 522 TLDAMTEIHEYNODLIRKQANKVKLSIVSLGTRSPQVPTCVDFVRPSNPWELAT 581
Qy 666 VFGAKELGKVVVDCCTDPDGR 686
Db 582 VFGAKELGKVVVDCCTDPDGR 602

RESULT 5

US-09-927-180-17
; Sequence 17, Application US/09927180
; Patent No. US20020106364A1

GENERAL INFORMATION:

APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA: US/09/927,180

APPLICATION NUMBER: US/09/927,180

FILING DATE: 09-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/519,223

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 394 amino acids

TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-927-180-17

Query Match 57.6%; Score 2084; DB 9; Length 394;
Best Local Similarity 100.0%; Pred. No. 4,1e-182;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MOFGRVNTVSGVNTLPSNPRVKEVAVADYTSRVRVEEQLLIFONTPTMDCVLV 60
Db 1 MOFGRVNTVSGVNTLPSNPRVKEVAVADYTSRVRVEEQLLIFONTPTMDCVLV 60
Qy 61 NPNRSQSGRFLFOLEADALVNFHOYSQQLPFYESSQVLAETVLOLTLIRNHP 120
Db 61 NPNRSQSGRFLFOLEADALVNFHOYSQQLPFYESSQVLAETVLOLTLIRNHP 120
Qy 121 SVAHLAVELGIRECFHRSIIISCANCAENEBECTPLHLACRKGDGEIIVELVOYCHTQMD 180
Db 121 SVAHLAVELGIRECFHRSIIISCANCAENEBECTPLHLACRKGDGEIIVELVOYCHTQMD 180
Qy 181 VTDYKGETVFNHVAQGDNSQVTLQIGRNAVAGLQVNNQGLTPHLACQIGQEMVRVL 240
Db 181 VTDYKGETVFNHVAQGDNSQVTLQIGRNAVAGLQVNNQGLTPHLACQIGQEMVRVL 240
Qy 241 LCNARCNIMGPNGYPIYSAMKFSQKGCAMTISMDSQIHSKDPYRGASPLHMAKNAEMA 300
Db 241 LCNARCNIMGPNGYPIYSAMKFSQKGCAMTISMDSQIHSKDPYRGASPLHMAKNAEMA 300
Qy 301 RMLLKRGCVNNTSSAGNTALHVGWVRNRPDCAIVLLTHGANADAGEHNTPLHMAK 360
Db 301 RMLLKRGCVNNTSSAGNTALHVGWVRNRPDCAIVLLTHGANADAGEHNTPLHMAK 360
Qy 361 DNVEIMKALIVGAEDVTNDPGEPTPLASKIG 394
Db 361 DNVEIMKALIVGAEDVTNDPGEPTPLASKIG 394

RESULT 6

US-09-927-180-19
; Sequence 19, Application US/09927180
; Patent No. US20020106364A1

GENERAL INFORMATION:

APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA: US/09/927,180

APPLICATION NUMBER: US/09/927,180

FILING DATE: 09-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/519,223

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 19:

QY 600 LLAANPTLDAMTEIHEYNODLIRKQANKYKLSIVSLGTGSPQVPTCVDFRSPNP 659
 DB 601 LLAANPTLDAMTEIHEYNODLIRKQANKYKLSIVSLGTGSPQVPTCVDFRSPNP 660
 QY 660 WEIAKTVFGAKEIGKMWVDDCCTDPDGR 687
 DB 661 WEIAKTVFGAKEIGKMWVDDCCTDPDGR 688

RESULT 3

US-09-927-180-2

; Sequence 2, Application US/09927180
 ; Patent No. US20020106364A1
 ; GENERAL INFORMATION:

APPLICANT: Jones, Simon
 Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.
 STREET: 87 Cambridgepark Drive
 CITY: Cambridge
 STATE: Massachusetts

COUNTRY: U.S.A.
 ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/927,180
 FILING DATE: 09-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/519,223
 FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.
 REGISTRATION NUMBER: 32,724

TELEPHONE: (617) 498-8224
 TELEFAX: (617) 498-8224

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 752 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-927-180-2

Query Match 91.2%; Score 3302.5; DB 9; Length 752;
 Best Local Similarity 90.4%; Pred. No. 1,76-293;

Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MOFGRLVNTFSQVTLNFSNPFYKEVAVADYTSDDRREKQILPONTNRTWDCVLV 60
 DB 1 MOFGRLVNTFSQVTLNFSNPFYKEISVADYTSHERREKQILPONSANRKTWDCVLV 60
 QY 61 NPNRSQGFRLFOLEADALVNFHQYSSQLLPFYESSPOVLAHTEVLQHLTDLIRNHPW 120
 DB 61 SPNPHSGFRFLFOLESEADALVNFQOFSQLPFYESSVOVLHTEVLQHLSDLRSHPSW 120
 QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACKRGDGEILVELVOYCHTQMD 180
 DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACKRGDSEILVELVOYCHQMD 180
 QY 181 VTQKGETVTHYAVQDGNQVQLDLGRNAVAGLNQVNNQGLPLHLACQGLKQEMAVLL 240
 DB 181 VTQKGETVTHYAVQDGNQVQLDLGRNAVAGLNQVNNQGLPLHLACQGLKQEMAVLL 240
 QY 241 VTQKGETVTHYAVQDGNQVQLDLGRNAVAGLNQVNNQGLPLHLACQGLKQEMAVLL 240

QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMTISMDSSQHSKDPYVGA SPLHAKNAEMA 300
 DB 241 LCNARCNIMGPNSGPPIHTAKFSQKCAEMTISMDSSQHSKDPYVGA SPLHAKNAEMA 300
 QY 301 RMLKRGCAVNSTSSAGNTALHVGVMNRFPDCAIVLLTGANDARGEHNTPLHLAMSK 360
 DB 301 RMLKRGCAVNSTSSAGNTALHVGVMNRFPDCAIVLLTGANDARGEHNTPLHLAMSK 360
 QY 361 DNMEMI KALIVFGAEVDTPNDFGETPFAFMASKISKQLQDIMPISRARKPAFILSMRDEK 419
 DB 361 DNMEMI KALIVFGAEVDTPNDFGETPFAFMASKISKQLQDIMPISRARKPAFILSMRDEK 420
 QY 420 RTDHLCLDGGGKGLIITQLIATEKASGAVTKDLFDVAVGNTGIIALALHRSKM 479
 DB 421 RHDHLCLDGGGKGLIITQLIATEKASGAVTKDLFDVAVGNTGIIALALHRSKM 480
 QY 480 AYKRGMYFRMKDEYFRSGRPYESGPLEEFLKREGEHTKMTDVKPKMYLTGTLSDQPA 539
 DB 481 AYKRGMYFRMKDEYFRSGRPYESGPLEEFLKREGEHTKMTDVKPKMYLTGTLSDQPA 540
 QY 540 ELHLFRNYDAPEVIREFRFNQVNLRRPAPSDQLVVRARSSGAAPTYFRPNGRFLDGG 599
 DB 541 ELHLFRNYDAPEVIREFRFNQVNLRRPAPSDQLVVRARSSGAAPTYFRPNGRFLDGG 600
 QY 600 LLAANPTLDAMTEIHEYNODLIRKQANKYKLSIVSLGTGSPQVPTCVDFRSPNP 659
 DB 601 LLAANPTLDAMTEIHEYNODLIRKQANKYKLSIVSLGTGSPQVPTCVDFRSPNP 660
 QY 660 WEIAKTVFGAKEIGKMWVDDCCTDPDGR 686
 DB 661 WEIAKTVFGAKEIGKMWVDDCCTDPDGR 687

RESULT 4

US-10-108-260A-3778

; Sequence 3778, Application US/10108260A
 ; Publication No. US20040005560A1
 ; GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: No. US20040005560A1el full length cDNA
 FILE REFERENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/10/108,260A

CURRENT FILING DATE: 2002-03-27

NUMBER OF SEQ ID NOS: 5458
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 3778

LENGTH: 667
 TYPE: PRT
 ORGANISM: Homo sapiens

US-10-108-260A-3778

Query Match 75.2%; Score 2723; DB 15; Length 667;
 Best Local Similarity 73.3%; Pred. No. 2,1e-240;
 Matches 543; Conservative 2; Mismatches 2; Indels 194; Gaps 2;

QY 1 MOFGRLVNTFSQVTLNFSNPFYKEVAVADYTSDDRREKQILPONTNRTWDCVLV 60
 DB 1 MOFGRLVNTFSQVTLNFSNPFYKEVAVADYTSDDRREKQILPONTNRTWDCVLV 60
 QY 61 NPNRSQGFRLFOLEADALVNFHQYSSQLLPFYESSPOVLAHTEVLQHLTDLIRNHPW 120
 DB 61 YPNRSQGFRLFOLEADALVNFHQYSS----- 89
 QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACKRGDGEILVELVOYCHTQMD 180
 DB 90 ----- 89
 QY 181 VTQKGETVTHYAVQDGNQVQLDLGRNAVAGLNQVNNQGLPLHLACQGLKQEMAVLL 240
 DB 90 ----- 101
 QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMTISMDSSQHSKDPYVGA SPLHAKNAEMA 300

LENGTH: 687 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 21:
 US-09-927-180-21

Query Match 100.0%; Score 3620; DB 9; Length 687;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFGRLVNTFSGVNTLFSNPRVKEVAADYTSDDRVBEGQLIFONTNPRMTDCVLY 60
 DB 1 MOFGRLVNTFSGVNTLFSNPRVKEVAADYTSDDRVBEGQLIFONTNPRMTDCVLY 60
 QY 61 NPNRSQSGRFLQLEADALVNFHQSQQLPFYESSQVLTETVLOHLTLIRNHPW 120
 DB 61 NPNRSQSGRFLQLEADALVNFHQSQQLPFYESSQVLTETVLOHLTLIRNHPW 120
 QY 121 SVAAHLAVELGIRECFHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTQMD 180
 DB 121 SVAAHLAVELGIRECFHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTQMD 180
 QY 181 VTDYKGETVFHYAVOGDNSQVLLGRNAVAGLNVNNGQLTPLHLACQLGQEWVRVLL 240
 DB 181 VTDYKGETVFHYAVOGDNSQVLLGRNAVAGLNVNNGQLTPLHLACQLGQEWVRVLL 240
 QY 241 LCNARCNIMGPNPGYPHSMKFSQKGCAMTISMSQSHSKDPRYGASPLHMAKNAEMA 300
 DB 241 LCNARCNIMGPNPGYPHSMKFSQKGCAMTISMSQSHSKDPRYGASPLHMAKNAEMA 300
 QY 301 RMLLRKGCNVNSTSSAGNTALHGVWRNRPDCAIVLLTHGANADARGHGNTPLHLAMSK 360
 DB 301 RMLLRKGCNVNSTSSAGNTALHGVWRNRPDCAIVLLTHGANADARGHGNTPLHLAMSK 360
 QY 361 DNVEMIKALIVGAEDVTENDFGETPTFLASKIGKLQDLMIH SRARKPAFIIGSRDEKR 420
 DB 361 DNVEMIKALIVGAEDVTENDFGETPTFLASKIGKLQDLMIH SRARKPAFIIGSRDEKR 420
 QY 421 TTDHLLCLDGGGVKGLITLQLLIAEKASGVAATKDLFDVAVAGTSTGGIALLAILHSKMA 480
 DB 421 TTDHLLCLDGGGVKGLITLQLLIAEKASGVAATKDLFDVAVAGTSTGGIALLAILHSKMA 480
 QY 481 YNRGMYFRMKDEVFRSGRPYESGPLEEFLKREFGHTKMTDVRKPKVMTLGTLSDRQPAE 540
 DB 481 YNRGMYFRMKDEVFRSGRPYESGPLEEFLKREFGHTKMTDVRKPKVMTLGTLSDRQPAE 540
 QY 541 LHLFRNYDAPETVREBRFNQVNLRRPAPSDQLVWRAARSSGAAPTYFRPNGRFLDGGI 600
 DB 541 LHLFRNYDAPETVREBRFNQVNLRRPAPSDQLVWRAARSSGAAPTYFRPNGRFLDGGI 600
 QY 601 LANNPLDAMTEIHEYNQDLIRKGOANKYKLSIVVSLGTGRSPQVPTCVDFRPSNFW 660
 DB 601 LANNPLDAMTEIHEYNQDLIRKGOANKYKLSIVVSLGTGRSPQVPTCVDFRPSNFW 660
 QY 661 ELAKTVFGAKELGKMWVDCCTDPDGRP 687
 DB 661 ELAKTVFGAKELGKMWVDCCTDPDGRP 687

RESULT 2
 US-09-927-180-23

Sequence 23, Application US/09927180
 Patent No. US20020106364A1

GENERAL INFORMATION:
 APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/927,180
 FILING DATE: 09-Aug-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/519,223
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Scott A.
 REGISTRATION NUMBER: 32,724
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 498-8224
 TELEFAX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 688 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 23:
 US-09-927-180-23

Query Match 99.6%; Score 3606.5; DB 9; Length 688;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MOFGRLVNTFSGVNTLFSNPRVKEVAADYTSDDRVBEGQLIFONTNPRMTDCVLY 60
 DB 1 MOFGRLVNTFSGVNTLFSNPRVKEVAADYTSDDRVBEGQLIFONTNPRMTDCVLY 60
 QY 61 NPNRSQSGRFLQLEADALVNFHQSQQLPFYESSQVLTETVLOHLTLIRNHPW 120
 DB 61 NPNRSQSGRFLQLEADALVNFHQSQQLPFYESSQVLTETVLOHLTLIRNHPW 120
 QY 121 SVAAHLAVELGIRECFHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTQMD 180
 DB 121 SVAAHLAVELGIRECFHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTQMD 180
 QY 181 VTDYKGETVFHYAVOGDNSQVLLGRNAVAGLNVNNGQLTPLHLACQLGQEWVRVLL 240
 DB 181 VTDYKGETVFHYAVOGDNSQVLLGRNAVAGLNVNNGQLTPLHLACQLGQEWVRVLL 240
 QY 241 LCNARCNIMGPNPGYPHSMKFSQKGCAMTISMSQSHSKDPRYGASPLHMAKNAEMA 300
 DB 241 LCNARCNIMGPNPGYPHSMKFSQKGCAMTISMSQSHSKDPRYGASPLHMAKNAEMA 300
 QY 301 RMLLRKGCNVNSTSSAGNTALHGVWRNRPDCAIVLLTHGANADARGHGNTPLHLAMSK 360
 DB 301 RMLLRKGCNVNSTSSAGNTALHGVWRNRPDCAIVLLTHGANADARGHGNTPLHLAMSK 360
 QY 361 DNVEMIKALIVGAEDVTENDFGETPTFLASKIGK-LQDLMIH SRARKPAFIIGSRDEKR 419
 DB 361 DNVEMIKALIVGAEDVTENDFGETPTFLASKIGK-LQDLMIH SRARKPAFIIGSRDEKR 420
 QY 421 TTDHLLCLDGGGVKGLITLQLLIAEKASGVAATKDLFDVAVAGTSTGGIALLAILHSKMA 480
 DB 421 TTDHLLCLDGGGVKGLITLQLLIAEKASGVAATKDLFDVAVAGTSTGGIALLAILHSKMA 480
 QY 480 AYRGMVFRMKDEVFRSGRPYESGPLEEFLKREFGHTKMTDVRKPKVMTLGTLSDRQPAE 539
 DB 480 AYRGMVFRMKDEVFRSGRPYESGPLEEFLKREFGHTKMTDVRKPKVMTLGTLSDRQPAE 540
 QY 540 ELHLFRNYDAPETVREBRFNQVNLRRPAPSDQLVWRAARSSGAAPTYFRPNGRFLDGG 599
 DB 540 ELHLFRNYDAPETVREBRFNQVNLRRPAPSDQLVWRAARSSGAAPTYFRPNGRFLDGG 600

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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:20:02 ; Search time 93.6667 Seconds
(without alignments)
2530.207 Million cell updates/sec

Title: US-10-612-668-21
Perfect score: 3620
Sequence: 1 MGFGRVLTVPFGVNLFSN.....GAKELGRNVVDCCTPDGRD 687

Scoring table: BLOSUM62
Gapop 10.0 , Gapec 0.5

Searched: 146209 segs, 344972447 residues
Total number of hits satisfying chosen parameters: 146209

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3620	100.0	687	US-09-927-180-21	Sequence 21, Appl
2	3606.5	99.6	688	US-09-927-180-23	Sequence 23, Appl
3	3302.5	91.2	752	US-09-927-180-2	Sequence 2, Appl
4	2723	75.2	667	US-10-108-260A-3778	Sequence 3778, Ap
5	2084	57.6	394	US-09-927-180-17	Sequence 17, Appl
6	1531	42.3	232	US-09-927-180-19	Sequence 19, Appl
7	647.5	17.9	1071	US-10-369-493-6865	Sequence 6865, Ap
8	634.5	17.5	1023	US-10-369-493-6689	Sequence 6689, Ap
9	634.5	17.5	1023	US-10-369-493-6690	Sequence 6690, Ap
10	324.5	9.0	468	US-10-369-493-4998	Sequence 4998, Ap
11	324	9.0	1330	US-10-108-260A-3237	Sequence 3237, Ap
12	302	8.3	786	US-10-164-080-2	Sequence 2, Appl
13	302	8.3	786	US-10-299-327-2	Sequence 2, Appl

14	302	8.3	786	14	US-10-128-174-13	Sequence 13, Appl
15	302	8.3	786	14	US-10-128-174-31	Sequence 31, Appl
16	302	8.3	786	14	US-10-128-174-32	Sequence 32, Appl
17	302	8.3	786	14	US-10-128-174-33	Sequence 33, Appl
18	302	8.3	787	10	US-09-866-050A-334	Sequence 334, App
19	301.5	8.3	347	14	US-10-128-174-30	Sequence 30, Appl
20	300.5	8.3	1724	9	US-09-964-899-43	Sequence 43, Appl
21	300	8.3	1762	14	US-10-205-194-117	Sequence 117, App
22	296	8.2	1094	17	US-10-479-764-22	Sequence 22, Appl
23	296	8.2	3913	15	US-10-334-143-42	Sequence 45, Appl
24	290	8.0	720	15	US-10-433-794-20	Sequence 20, Appl
25	290	8.0	765	14	US-10-128-174-3	Sequence 3, Appl
26	290	8.0	765	14	US-10-128-174-34	Sequence 34, Appl
27	290	8.0	765	14	US-10-128-174-35	Sequence 35, Appl
28	290	8.0	765	14	US-10-128-174-36	Sequence 36, Appl
29	290	8.0	765	14	US-10-128-174-37	Sequence 37, Appl
30	290	8.0	765	14	US-10-128-174-38	Sequence 38, Appl
31	290	8.0	765	14	US-10-128-174-39	Sequence 39, Appl
32	290	8.0	765	14	US-10-128-174-40	Sequence 40, Appl
33	290	8.0	765	14	US-10-128-174-41	Sequence 41, Appl
34	290	8.0	765	14	US-10-128-174-42	Sequence 42, Appl
35	290	8.0	765	14	US-10-128-174-43	Sequence 43, Appl
36	290	8.0	765	14	US-10-128-174-44	Sequence 44, Appl
37	290	8.0	765	15	US-10-182-243-56	Sequence 56, Appl
38	284.5	7.9	784	14	US-10-164-080-7	Sequence 7, Appl
39	284.5	7.9	784	15	US-10-258-951-70	Sequence 70, Appl
40	282.5	7.8	784	14	US-10-354-358-38	Sequence 38, Appl
41	282.5	7.8	784	14	US-10-128-174-12	Sequence 12, Appl
42	282.5	7.8	784	14	US-10-658-904-2	Sequence 2, Appl
43	279.5	7.7	784	16	US-10-648-593-153	Sequence 153, App
44	278.5	7.7	1053	15	US-10-291-172-343	Sequence 343, App
45	278.5	7.7	1053	15	US-10-221-278-343	Sequence 343, App

ALIGNMENTS

RESULT 1
US-09-927-180-21
Sequence 21, Application US/09927180
Patent No. US20020106364A1
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:

QY 241 LCNARCNMGNGYPPIHSAMKESQKGCAMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNMGNGSPGPIHTAMKESQKGCAMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRGCNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRGCNDVSTSAAGNTALHVAVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDPNDGTPFLASKIGIQLQDLMPISRAKPAFISLSSNRDEK 420
DB 361 DNVEIMKALIVFGAEVDTNDPNDGTPFLASKIGIQLQDLMPISRAKPAFISLSSNRDEK 420
QY 421 RTHDLHLCLDGGVGLIIIIQLLIAIEKASGVATKDLFDWVAGTSGGILALAILHLSKM 480
DB 421 RTHDLHLCLDGGVGLIIIIQLLIAIEKASGVATKDLFDWVAGTSGGILALAILHLSKM 480
QY 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMTLGTLSDRQPA 540
DB 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMTLGTLSDRQPA 540
QY 541 ELHLFRNYDAPETVREPRNQNVNLRPPAOPSDQLVWRAARSSGAAPTFRPNRFLDGG 600
DB 541 ELHLFRNYDAPETVREPRNQNVNLRPPAOPSDQLVWRAARSSGAAPTFRPNRFLDGG 600
QY 601 LIANPTLDAMTEIHEYNODLIRKGOANKVKLSIIVSLGTGRSPQVPVTCVDVFRPSNP 660
DB 601 LIANPTLDAMTEIHEYNODLIRKGOANKVKLSIIVSLGTGRSPQVPVTCVDVFRPSNP 660
QY 661 WELAKTVFGAKELGKMWVDCCTDPCR 687
DB 661 WELAKTVFGAKELGKMWVDCCTDPCR 687

RESULT 15

US-08-555-568B-17
; Sequence 17, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-17

Query Match

57.5%; Score 2084; DB 2; Length 394;

Best Local Similarity 100.0%; Pred. No. 1.9e-216;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQFFGRLVNTFSGVTNLFSPNFRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGRLVNTFSGVTNLFSPNFRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSFRLLFQLEADALVNFHOYSQQLLPFYESSPOVLHTEVLOHLTDLIRNHPSW 120
DB 61 NPNRSQSFRLLFQLEADALVNFHOYSQQLLPFYESSPOVLHTEVLOHLTDLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEIILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEIILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNMGNGYPPIHSAMKESQKGCAMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNMGNGYPPIHSAMKESQKGCAMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRGCNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRGCNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDPNDGTPFLASKIG 394
DB 361 DNVEIMKALIVFGAEVDTNDPNDGTPFLASKIG 394

Search completed: May 26, 2005, 14:22:02
Job time : 28.3702 secs

[illegible][illegible]

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-2

Query Match
Best Local Similarity 91.4%; Score 3315; DB 2; Length 752;
Matches 621; Conservative 32; Mismatches 34; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTSGVNTLFSNPRVKEVAVADYTSDDRVREEGQLILFQNTPTNRTWDCVILV 60
Db 1 MOFFGRLVNTLSSVNTLFSNPRVKEISVADYTSHERVREEGQLILFQNASRNTWDCILV 60
QY 61 NPNRSQSGLRLEADALVNFHQSOLLPFYESSQVLTHTVQLHLDLIRNHPWS 120
Db 61 SPRNHSGLRLEADALVNFQSSQLPFYESSQVLTHTVQLHLDLIRNHPWS 120
QY 121 SYAHVALVGLIGRECFHSHRSIIISCANSTENEGCTPLHLACRGDGEILVELVOYCHTQMD 180
Db 121 TVTHLAVELIGRECFHSHRSIIISCANSTENEGCTPLHLACRGDGEILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLQLGRNAVAGLNQVNNQGLTPLHLACQMGQEMVRVLL 240
Db 181 VTDNKGETAFAHYAVQGDNSQVLLQLGRNAVAGLNQVNNQGLTPLHLACQMGQEMVRVLL 240
QY 361 DNVMEMIKALIVFGAEVDTNDFGCTPTFLASKIGRQLQDLMIHSRARKPAFILGSMRDEK 420
Db 361 DNWEMIKALIVFGAEVDTNDFGCTPTFAWASKISKQLQDLMIHSRARKPAFILGSMRDEK 420
QY 421 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGILALAILHKSMM 480
Db 421 RIHDLHLLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGILALAILHKSMM 480
QY 481 AYMRGMVFRMKDEVFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMTLGTSLDRQPA 540
Db 481 AYMRGVYFRMKDEVFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMTLGTSLDRQPA 540
QY 541 ELHLFRNYDAPETVREPRENQNVNLRPPAQPSDQLVWRAARSSGAAPTFRPNRFLDGG 600
Db 541 ELHLFRNYDAPETVREPRENQNVNLRPPAQPSDQLVWRAARSSGAAPTFRPNRFLDGG 600
QY 601 LLANNPTLDAMTEIHEYNDLIRKQGNKVKLSIIVSLGTGRSPQVPTCYDVFPPSPNP 660
Db 601 LLANNPTLDAMTEIHEYNDLIRKQGNKVKLSIIVSLGTGRSPQVPTCYDVFPPSPNP 660
QY 661 WELAKTVFGAKELGKMWVDCCTDPPGR 687
Db 661 WELAKTVFGAKELGKMWVDCCTDPPGR 687

RESULT 12
US-09-519-223-2
Sequence 2, Application US/09519223
Patent No. 6274140
GENERAL INFORMATION:
APPLICANT: Jones, Simon
APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-519-223-2

Query Match
Best Local Similarity 91.4%; Score 3315; DB 3; Length 752;
Matches 621; Conservative 32; Mismatches 34; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTSGVNTLFSNPRVKEVAVADYTSDDRVREEGQLILFQNTPTNRTWDCVILV 60
Db 1 MOFFGRLVNTLSSVNTLFSNPRVKEISVADYTSHERVREEGQLILFQNASRNTWDCILV 60
QY 61 NPNRSQSGLRLEADALVNFHQSOLLPFYESSQVLTHTVQLHLDLIRNHPWS 120
Db 61 SPRNHSGLRLEADALVNFQSSQLPFYESSQVLTHTVQLHLDLIRNHPWS 120
QY 121 SYAHVALVGLIGRECFHSHRSIIISCANSTENEGCTPLHLACRGDGEILVELVOYCHTQMD 180
Db 121 TVTHLAVELIGRECFHSHRSIIISCANSTENEGCTPLHLACRGDGEILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLQLGRNAVAGLNQVNNQGLTPLHLACQMGQEMVRVLL 240
Db 181 VTDNKGETAFAHYAVQGDNSQVLLQLGRNAVAGLNQVNNQGLTPLHLACQMGQEMVRVLL 240
QY 241 LCNARCNIIMPNGYPYIHSAMKFSQKCAEMIIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNIIMPNGYPYIHSAMKFSQKCAEMIIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRGCVNNTSSAGNTALHVGWVRNRFDCALVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLKRGCVNNTSSAGNTALHVGWVRNRFDCALVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVMEMIKALIVFGAEVDTNDFGCTPTFLASKIGRQLQDLMIHSRARKPAFILGSMRDEK 420
Db 361 DNWEMIKALIVFGAEVDTNDFGCTPTFAWASKISKQLQDLMIHSRARKPAFILGSMRDEK 420
QY 421 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGILALAILHKSMM 480
Db 421 RIHDLHLLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGILALAILHKSMM 480
QY 481 AYMRGMVFRMKDEVFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMTLGTSLDRQPA 540
Db 481 AYMRGVYFRMKDEVFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMTLGTSLDRQPA 540
QY 541 ELHLFRNYDAPETVREPRENQNVNLRPPAQPSDQLVWRAARSSGAAPTFRPNRFLDGG 600
Db 541 ELHLFRNYDAPETVREPRENQNVNLRPPAQPSDQLVWRAARSSGAAPTFRPNRFLDGG 600
QY 601 LLANNPTLDAMTEIHEYNDLIRKQGNKVKLSIIVSLGTGRSPQVPTCYDVFPPSPNP 660
Db 601 LLANNPTLDAMTEIHEYNDLIRKQGNKVKLSIIVSLGTGRSPQVPTCYDVFPPSPNP 660

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QY 301 RMLLKRGCVNNTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGNTPHLHLSK 360
DB 301 RMLLKRGCDVDSTSAAGNTALHVAVMNRFDCAIVLLTHGANADARGEHGNTPHLHLSK 360
QY 361 DNVEMLKALVFGAEVDTPNDGFTPTFLASKIGROLQDLMPISRAARKPAFILSSMRDEK 420
DB 361 DNVEMLKALVFGAEVDTPNDGFTPTFLASKIGROLQDLMPISRAARKPAFILSSMRDEK 420
QY 421 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKOLFVWAGTSTGGILALAILHLSKSM 480
DB 421 RIHDHLLCLDGGVKGVLIIQLLIAIEKASGVATKOLFVWAGTSTGGILALAILHLSKSM 480
QY 481 AYMRGMVFRMKDEVFGRSRYESGPLEEFLKREFGHTKMTDVRKPKVMLTGTLSRQPA 540
DB 481 AYMRGMVFRMKDEVFGRSRYESGPLEEFLKREFGHTKMTDVRKPKVMLTGTLSRQPA 540
QY 541 ELHLFRNYDAPETVREPRFNQNLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 600
DB 541 ELHLFRNYDAPETVREPRFNQNLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 600
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DB 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
QY 661 WELAKTVFGAKELGKMVDDCCTDPDGR 687
DB 661 WELAKTVFGAKELGKMVDDCCTDPDGR 687

RESULT 10

US-08-735-716-2
; Sequence 2, Application US/08735716
; Patent No. 5840511
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735, 716
; FILING DATE: 23-OCT-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-735-716-2

Query Match 91.4%; Score 3315; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 32; Mismatches 34; Indels 0; Gaps 0;

QY 1 MQFFGLVNTFFSGVTNLFNSPPFVKEVAVADYTSRDRVEEGQLILFONTPNRTWCVLV 60
DB 1 MQFFGLVNTSSVTNLFNSPPFVKEISVADYTSHERVREEGQLILFONASNRTWCVLV 60
QY 61 NPNRSGFRLFOLEADALNVFHOVSSOLLPFYESSPOVLHTEVLQHLTDLIRNHPW 120
DB 61 SPNPHSGFRLFOLEADALNVFQFSSQLPFYESSQVQLHVEVLQHLSDLIRHPW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENBEGCTPLHLACKRGDGIIVELVOYCHTQMD 180
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENBEGCTPLHLACKRGDSEILVELVOYCHAQMD 180

QY 181 VTDKGETVFHYAVQGDNSQVLLQLLGRNAVAGLNQVNNQGLTPLHLACQLCKQEMVRVLL 240
DB 181 VTDKGETAFHYAVQGDNSQVLLQLLGKVASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
QY 241 LCNARNCINMGPNPYTHSAMKFSQKCAEMIIISWDSSQIHSKOPRYGASPLHWAKNAEMA 300
DB 241 LCNARNCINMGPNPYTHSAMKFSQKCAEMIIISWDSSQIHSKOPRYGASPLHWAKNAEMA 300
QY 301 RMLLKRGCVNNTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGNTPHLHLSK 360
DB 301 RMLLKRGCDVDSTSAAGNTALHVAVMNRFDCAIVLLTHGANADARGEHGNTPHLHLSK 360
QY 361 DNVEMLKALVFGAEVDTPNDGFTPTFLASKIGROLQDLMPISRAARKPAFILSSMRDEK 420
DB 361 DNVEMLKALVFGAEVDTPNDGFTPTFLASKIGROLQDLMPISRAARKPAFILSSMRDEK 420
QY 421 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKOLFVWAGTSTGGILALAILHLSKSM 480
DB 421 RIHDHLLCLDGGVKGVLIIQLLIAIEKASGVATKOLFVWAGTSTGGILALAILHLSKSM 480
QY 481 AYMRGMVFRMKDEVFGRSRYESGPLEEFLKREFGHTKMTDVRKPKVMLTGTLSRQPA 540
DB 481 AYMRGMVFRMKDEVFGRSRYESGPLEEFLKREFGHTKMTDVRKPKVMLTGTLSRQPA 540
QY 541 ELHLFRNYDAPETVREPRFNQNLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 600
DB 541 ELHLFRNYDAPETVREPRFNQNLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 600
QY 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
DB 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
QY 661 WELAKTVFGAKELGKMVDDCCTDPDGR 687
DB 661 WELAKTVFGAKELGKMVDDCCTDPDGR 687

RESULT 11

US-08-555-568B-2
; Sequence 2, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid

QY 547 NYDAPETVREPRFNQVNLPPAQRSDQLVWRAARSSGAAPTYFRPNGRFLDGGLLANPP 606
 DB 614 NYDAPETVREPRFNQVNLPPAQRSDQLVWRAARSSGAAPTYFRPNGRFLDGGLLANPP 673
 QY 607 TLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPNPNWELAKT 666
 DB 674 TLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPNPNWELAKT 733
 QY 667 VEGAKELGKMWVDCCTDPDGR 687
 DB 734 VEGAKELGKMWVDCCTDPDGR 754
 RESULT 8
 US-08-281-193-2
 ; Sequence 2, Application US/08281193
 ; Patent No. 5466595
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; APPLICANT: Tang, Jim
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 15
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/281,193
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 752 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-281-193-2
 Query Match 91.4%; Score 3315; DB 1; Length 752;
 Best Local Similarity 90.4%; Pred. No. 0;
 Matches 621; Conservative 32; Mismatches 34; Indels 0; Gaps 0;
 QY 1 MQFFGRLVNTFGVNTLFSNPRFRVKEVADYTSDDRVREEGQLILFQNTNRTWDCVILV 60
 DB 1 MQFFGRLVNTLSSVNTLFSNPRFRVKEISVADYTSHERVREEGQLILFQNASRNTWDCILV 60
 QY 61 NPNRSQSGRFLQLEADALVNFHQYSSQLLPFFYESSQVQLHVEVLQHLTLIRNHPWS 120
 DB 61 SPRNPHSGRFLQLESEADALVNFQFSSQLPPFYESSQVQLHVEVLQHLSDLIRSHPSW 120
 QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDSILVELVOYCHTQMD 180
 DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRKGDSILVELVOYCHAQMD 180
 QY 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMVRVLL 240
 DB 181 VTDNKGETAFAHYAVQGDNSQVQLLGNKASAGLNQVNNQGLTPHLACQMGKQEMVRVLL 240
 QY 241 LCNARCNIMGPNGYPIHSAKFSQKCAEWIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
 DB 241 LCNARCNVMPGSGFPPIHTAMKFSQKCAEWIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
 QY 301 RMLKKGCVNSTSSAGNTALHVGVMNRNFDCAIALLTHGANADARGEHNTPLHLAMSK 360
 DB 301 RMLKKGCDVDSTSAAGNTALHVAVMNRNFDCAIALLTHGANAGTCEHNTPLHLAISK 360
 QY 361 DNWEMIKALIVFGAEVDTNDFTETPTFLASKIGRQLQDLMIHSRARKPAFILGSMRDEK 420
 DB 361 DNWEMIKALIVFGAEVDTNDFTETPAFWASKISKQLQDLMLPSRARKPAFILSSMRDEK 420
 QY 421 RTHDHLCLDGGVKGGLIIQLLIAIEKASGVATKOLFOWVAGTSTGGILALAILHKSXM 480

DB 421 RIHDHLLCLDGGVKGGLVLIQLLIAIEKASGVATKOLFOWVAGTSTGGILALAILHKSXM 480
 QY 481 AYMRGMVFRMKDEVPFRGSRPYESGPLEBFLKREBFEHTKMTDVRKPKVMLTGLTSLDRQPA 540
 DB 481 AYMRGMVFRMKDEVPFRGSRPYESGPLEBFLKREBFEHTKMTDVRKPKVMLTGLTSLDRQPA 540
 QY 541 ELHLFRNYDAPETVREPRFNQVNLPPAQRSDQLVWRAARSSGAAPTYFRPNGRFLDGG 600
 DB 541 ELHLFRNYDAPETVREPRFNQVNLPPAQRSDQLVWRAARSSGAAPTYFRPNGRFLDGG 600
 QY 601 LIANNPTLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPNPNWELAKT 660
 DB 601 LIANNPTLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPNPNWELAKT 660
 QY 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687
 DB 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687
 RESULT 9
 US-08-422-106-2
 ; Sequence 2, Application US/08422106
 ; Patent No. 5589170
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; APPLICANT: Tang, Jim
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 15
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/422,106
 ; FILING DATE: 14-APR-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/281,193
 ; FILING DATE: 27-JUL-1994
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 752 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-422-106-2
 Query Match 91.4%; Score 3315; DB 1; Length 752;
 Best Local Similarity 90.4%; Pred. No. 0;
 Matches 621; Conservative 32; Mismatches 34; Indels 0; Gaps 0;
 QY 1 MQFFGRLVNTFGVNTLFSNPRFRVKEVADYTSDDRVREEGQLILFQNTNRTWDCVILV 60
 DB 1 MQFFGRLVNTLSSVNTLFSNPRFRVKEISVADYTSHERVREEGQLILFQNASRNTWDCILV 60
 QY 61 NPNRSQSGRFLQLEADALVNFHQYSSQLLPFFYESSQVQLHVEVLQHLTLIRNHPWS 120
 DB 61 SPRNPHSGRFLQLESEADALVNFQFSSQLPPFYESSQVQLHVEVLQHLSDLIRSHPSW 120
 QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDSILVELVOYCHTQMD 180
 DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRKGDSILVELVOYCHAQMD 180
 QY 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMVRVLL 240
 DB 181 VTDNKGETAFAHYAVQGDNSQVQLLGNKASAGLNQVNNQGLTPHLACQMGKQEMVRVLL 240
 QY 241 LCNARCNIMGPNGYPIHSAKFSQKCAEWIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
 DB 241 LCNARCNVMPGSGFPPIHTAMKFSQKCAEWIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match 99.5%; Score 3606.5; DB 4; Length 687;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MQFFGRLVNTFSGVTNLFNSNPFVRKVEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGRLVNTFSGVTNLFNSNPFVRKVEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60

QY 61 NPNRSOSGRLFOLELEADALVNFHOYSQQLLPFYESSQVLHTEVLOHLTDLIRNHPWS 120
DB 61 NPNRSOSGRLFOLELEADALVNFHOYSQQLLPFYESSQVLHTEVLOHLTDLIRNHPWS 120

QY 121 SVAHLAVALGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDDGILVELVOYCHTQMD 180
DB 121 SVAHLAVALGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDDGILVELVOYCHTQMD 180

QY 181 VTDYKGETVFHYAVQDGNQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQDGNQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240

QY 241 LCNARCNIINGPNGYPYTHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIINGPNGYPYTHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300

QY 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360

QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 420
DB 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 419

QY 421 RTHDHLCLDGGVKGKLIILQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMM 480
DB 420 RTHDHLCLDGGVKGKLIILQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMM 479

QY 481 AYMRGMVFRMKDVRFRGSRPYESGPLEEFLEKRFEGEHTKMTDVRKPKVMTGTLSDRQPA 540
DB 480 AYMRGMVFRMKDVRFRGSRPYESGPLEEFLEKRFEGEHTKMTDVRKPKVMTGTLSDRQPA 539

QY 541 ELHLFRNYDAPETVREPRNQNVNLRPPAPQPSQLVWRAARSGGAAPTFRPNRGFLDGG 600
DB 540 ELHLFRNYDAPETVREPRNQNVNLRPPAPQPSQLVWRAARSGGAAPTFRPNRGFLDGG 599

QY 601 LLANNPTLDAMTEIHEYNDLIRKGOANKVKKLSIVVSLGTGRSPQVPTCDVDFRPSNP 660
DB 600 LLANNPTLDAMTEIHEYNDLIRKGOANKVKKLSIVVSLGTGRSPQVPTCDVDFRPSNP 659

QY 661 WELAKTVFGAKELGKGMVVDCCDTPDGRP 688
DB 660 WELAKTVFGAKELGKGMVVDCCDTPDGRP 687

RESULT 7
US-09-949-016-10948
Sequence 10948, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10948
LENGTH: 819
TYPE: PRT
ORGANISM: Human
US-09-949-016-10948

Query Match 98.5%; Score 3572; DB 4; Length 819;
Best Local Similarity 92.4%; Pred. No. 0;
Matches 685; Conservative 1; Mismatches 1; Indels 54; Gaps 1;

QY 1 MQFFGRLVNTFSGVTNLFNSNPFVRKVEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 14 MQFFGRLVNTFSGVTNLFNSNPFVRKVEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 73

QY 61 NPNRSOSGRLFOLELEADALVNFHOYSQQLLPFYESSQVLHTEVLOHLTDLIRNHPWS 120
DB 74 NPNRSOSGRLFOLELEADALVNFHOYSQQLLPFYESSQVLHTEVLOHLTDLIRNHPWS 133

QY 121 SVAHLAVALGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDDGILVELVOYCHTQMD 180
DB 134 SVAHLAVALGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDDGILVELVOYCHTQMD 193

QY 181 VTDYKGETVFHYAVQDGNQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 194 VTDYKGETVFHYAVQDGNQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 253

QY 241 LCNARCNIINGPNGYPYTHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 254 LCNARCNIINGPNGYPYTHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 313

QY 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 314 RMLLKRCGNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 373

QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGR----- 395
DB 374 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGRLVTRKAILTLRTVGAECYCFPIHG 433

QY 396 -----OLQDLMIHSRARKPAFILGSMRDEKRTDHL 426
DB 434 VPAEQSSAAPHHPFSLERAQPPPISLNNLEQLQDLMIHSRARKPAFILGSMRDEKRTDHL 493

QY 427 LCLDGGVKGKLIILQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMMAYMRGM 486
DB 494 LCLDGGVKGKLIILQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMMAYMRGM 553

QY 487 YFRMKDEVFRGSRPYESGPLEEFLEKRFEGEHTKMTDVRKPKVMTGTLSDRQPAELHLFR 546
DB 554 YFRMKDEVFRGSRPYESGPLEEFLEKRFEGEHTKMTDVRKPKVMTGTLSDRQPAELHLFR 613

QY 241 LCNARCNMGNGYPIHSAKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHAKNAEMA 300
DB 241 LCNARCNMGNGYPIHSAKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHAKNAEMA 300
QY 301 RMLLKRCNCNVNSTSSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCNCNVNSTSSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDEGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 420
DB 361 DNVEIMKALIVFGAEVDTNDEGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 419
QY 421 RTHDHLCLDGGVKGKLIIOILLIAIEKASGVATKDLFDWAGTSGGILALAILHLSKSM 480
DB 420 RTHDHLCLDGGVKGKLIIOILLIAIEKASGVATKDLFDWAGTSGGILALAILHLSKSM 479
QY 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFKREFEGHTKMTDVRKPKVMLTGTLSDRQPA 540
DB 480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFKREFEGHTKMTDVRKPKVMLTGTLSDRQPA 539
QY 541 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDQVWRAARSSGAAPTFRPNRFLDGG 600
DB 540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDQVWRAARSSGAAPTFRPNRFLDGG 599
QY 601 LLANNPTLDAMTEIHEYNDLIRKGOANKVKKLSIIVSLGTGRSPQVPTCVDVFRPSNP 660
DB 600 LLANNPTLDAMTEIHEYNDLIRKGOANKVKKLSIIVSLGTGRSPQVPTCVDVFRPSNP 659
QY 661 WELAKTVFGAKELGKMWVDCCTDPDGRP 688
DB 660 WELAKTVFGAKELGKMWVDCCTDPDGRP 687

RESULT 5

US-09-519-223-21
; Sequence 21, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-519-223-21
Query Match 99.5%; Score 3606.5; DB 3; Length 687;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 MOFFGRLVNTSGVNTLFSNPRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVILV 60
DB 1 MOFFGRLVNTSGVNTLFSNPRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVILV 60
QY 61 NPNRSQSQRFLQFLEADALVNFHQYSSQLLPFYESSQVLHTEVQLHTLDIRNHPSW 120
DB 61 NPNRSQSQRFLQFLEADALVNFHQYSSQLLPFYESSQVLHTEVQLHTLDIRNHPSW 120
QY 121 SVAHLAVELGIRECFHHHSRIISCANCAENEBECTPLHLACRKGDSGEILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHHSRIISCANCAENEBECTPLHLACRKGDSGEILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVOGDNSQVLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVOGDNSQVLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNMGNGYPIHSAKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHAKNAEMA 300
DB 241 LCNARCNMGNGYPIHSAKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHAKNAEMA 300
QY 301 RMLLKRCNCNVNSTSSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCNCNVNSTSSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDEGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 420
DB 361 DNVEIMKALIVFGAEVDTNDEGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 419
QY 421 RTHDHLCLDGGVKGKLIIOILLIAIEKASGVATKDLFDWAGTSGGILALAILHLSKSM 480
DB 420 RTHDHLCLDGGVKGKLIIOILLIAIEKASGVATKDLFDWAGTSGGILALAILHLSKSM 479
QY 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFKREFEGHTKMTDVRKPKVMLTGTLSDRQPA 540
DB 480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFKREFEGHTKMTDVRKPKVMLTGTLSDRQPA 539
QY 541 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDQVWRAARSSGAAPTFRPNRFLDGG 600
DB 540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDQVWRAARSSGAAPTFRPNRFLDGG 599
QY 601 LLANNPTLDAMTEIHEYNDLIRKGOANKVKKLSIIVSLGTGRSPQVPTCVDVFRPSNP 660
DB 600 LLANNPTLDAMTEIHEYNDLIRKGOANKVKKLSIIVSLGTGRSPQVPTCVDVFRPSNP 659
QY 661 WELAKTVFGAKELGKMWVDCCTDPDGRP 688
DB 660 WELAKTVFGAKELGKMWVDCCTDPDGRP 687

RESULT 6

US-09-927-180-21
; Sequence 21, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

QY	ELHLPFRNYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRPNCGRFLDGG	600
Db	ELHLPFRNYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRPNCGRFLDGG	600
QY	LLANNPITLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVQVTCVDFRPSNP	660
Db	LLANNPITLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVQVTCVDFRPSNP	660
QY	WELAKTVFGAKELGKMWVDDCCTDDPDRP	688
Db	WELAKTVFGAKELGKMWVDDCCTDDPDRP	688
<p>RESULT 4</p> <p>US-08-555-5688-21</p> <p>; Sequence 21, Application US/0855555688</p> <p>; Patent No. 5976854</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Jones, Simon</p> <p>; APPLICANT: Tang, Jim</p> <p>; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B</p> <p>; NUMBER OF SEQUENCES: 25</p> <p>; CORRESPONDENCE ADDRESS:</p> <p>; ADDRESSEE: Genetics Institute, Inc.</p> <p>; STREET: 87 CambridgePark Drive</p> <p>; CITY: Cambridge</p> <p>; STATE: Massachusetts</p> <p>; COUNTRY: U.S.A.</p> <p>; ZIP: 02140</p> <p>; COMPUTER READABLE FORM:</p> <p>; MEDIUM TYPE: Floppy disk</p> <p>; OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)</p> <p>; CURRENT APPLICATION DATA:</p> <p>; APPLICATION NUMBER: US/08/555,568B</p> <p>; FILING DATE:</p> <p>; CLASSIFICATION: 435</p> <p>; ATTORNEY/AGENT INFORMATION:</p> <p>; NAME: Brown, Scott A.</p> <p>; REGISTRATION NUMBER: 32,724</p> <p>; TELECOMMUNICATION INFORMATION:</p> <p>; TELEPHONE: (617) 498-8224</p> <p>; TELEFAX: (617) 876-5851</p> <p>; INFORMATION FOR SEQ ID NO: 21:</p> <p>; SEQUENCE CHARACTERISTICS:</p> <p>; LENGTH: 688 amino acids</p> <p>; TYPE: amino acid</p> <p>; TOPOLOGY: linear</p> <p>; MOLECULE TYPE: protein</p> <p>; US-08-555-5688-21</p> <p>Query Match 99.5%; Score 3606.5; DB 2; Length 687;</p> <p>Best Local Similarity 99.7%; Pred. No. 0;</p> <p>Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;</p>		
QY	1 MQPFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREGQLILFQNTNRTWDCVLV	60
Db	1 MQPFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREGQLILFQNTNRTWDCVLV	60
QY	61 NPNRSQSGRLFOLEADALVNFHQYSSQLLPFYESSPQVLHTEVQLHLDLIRNHPWS	120
Db	61 NPNRSQSGRLFOLEADALVNFHQYSSQLLPFYESSPQVLHTEVQLHLDLIRNHPWS	120
QY	121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEIILVELVQYCHTQMD	180
Db	121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEIILVELVQYCHTQMD	180
QY	181 VTDYKGETVFHYAVQDGNQVLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL	240
Db	181 VTDYKGETVFHYAVQDGNQVLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL	240
<p>Query Match 99.5%; Score 3606.5; DB 2; Length 687;</p> <p>Best Local Similarity 99.7%; Pred. No. 0;</p> <p>Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;</p>		
QY	1 MQPFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREGQLILFQNTNRTWDCVLV	60
Db	1 MQPFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREGQLILFQNTNRTWDCVLV	60
QY	61 NPNRSQSGRLFOLEADALVNFHQYSSQLLPFYESSPQVLHTEVQLHLDLIRNHPWS	120
Db	61 NPNRSQSGRLFOLEADALVNFHQYSSQLLPFYESSPQVLHTEVQLHLDLIRNHPWS	120
QY	121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEIILVELVQYCHTQMD	180
Db	121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEIILVELVQYCHTQMD	180
QY	181 VTDYKGETVFHYAVQDGNQVLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL	240
Db	181 VTDYKGETVFHYAVQDGNQVLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL	240
QY	241 LCNARCNIMGPNYPHISAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA	300
Db	241 LCNARCNIMGPNYPHISAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA	300
QY	301 RMLLKRCGNVNTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGHGNTPPLHLAMSK	360
Db	301 RMLLKRCGNVNTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGHGNTPPLHLAMSK	360
QY	361 DNVEMLKALIVGAEDVTNDPFGTPTFLASKIGRQLQDLMIHSRKPAPFILGSMRDEK	420
Db	361 DNVEMLKALIVGAEDVTNDPFGTPTFLASKIGRQLQDLMIHSRKPAPFILGSMRDEK	420
QY	421 RTHDHLCLDGGGVKGLIIQLLAIERKASGVATKDLFDWAGTSTGGILALAILHKSMM	480
Db	421 RTHDHLCLDGGGVKGLIIQLLAIERKASGVATKDLFDWAGTSTGGILALAILHKSMM	480
QY	481 AYNRGMVFRMKQEVFRGSRPYESGPLEEFKREFGCHTKMTDVRKPKVMTGLTSDRQPA	540
Db	481 AYNRGMVFRMKQEVFRGSRPYESGPLEEFKREFGCHTKMTDVRKPKVMTGLTSDRQPA	540

QY 121 SVAHLAVELGIRECFHSHRIISCAENCAENEGCTPLHLACRKGDEILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHSHRIISCAENCAENEGCTPLHLACRKGDEILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNYPIHSAKESQKGAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEWA 300
DB 241 LCNARCNIMGPNYPIHSAKESQKGAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEWA 300
QY 301 RMLLRGCNVNSTSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRGCNVNSTSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDPGETPTFLASKIGRQLOQLMHI SRARKPAFILGSMRDEK 420
DB 361 DNVEIMKALIVFGAEVDTNDPGETPTFLASKIGRQLOQLMHI SRARKPAFILGSMRDEK 420
QY 421 RTHDHLCLDGGVKGGLIIIIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHLSKSM 480
DB 421 RTHDHLCLDGGVKGGLIIIIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHLSKSM 480
QY 481 AYMRGMVFRMKDEVFGRSGRPYSGPLEEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPA 540
DB 481 AYMRGMVFRMKDEVFGRSGRPYSGPLEEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPA 540
QY 541 ELHLFRNYDAPETVREPRFNQVNNLRPPAQPDSQLVWRAARSSGAAPTFRPNRFLDGG 600
DB 541 ELHLFRNYDAPETVREPRFNQVNNLRPPAQPDSQLVWRAARSSGAAPTFRPNRFLDGG 600
QY 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIIVSLGTRSPQVPTCDVFRPSNP 660
DB 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIIVSLGTRSPQVPTCDVFRPSNP 660
QY 661 WELAKTVFGAKELGKMWVDDCCTDDPGRP 688
DB 661 WELAKTVFGAKELGKMWVDDCCTDDPGRP 688

RESULT 2

US-09-519-223-23
; Sequence 23, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 498-8824
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-519-223-23

Query Match 100.0%; Score 3625; DB 3; Length 688;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 688; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTSGVTNLFSPRVKEVAVADYTSDDRVREEQQLILFQNTPNRTWDCVLLV 60
DB 1 MOFFGRLVNTSGVTNLFSPRVKEVAVADYTSDDRVREEQQLILFQNTPNRTWDCVLLV 60
QY 61 NPNRSQSGFRLLFQLEADALVNFHQSOLLPPFYESSPOVLHTEVQLHLTDLIRNHPSW 120
DB 61 NPNRSQSGFRLLFQLEADALVNFHQSOLLPPFYESSPOVLHTEVQLHLTDLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHSHRIISCAENCAENEGCTPLHLACRKGDEILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHSHRIISCAENCAENEGCTPLHLACRKGDEILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNYPIHSAKESQKGAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEWA 300
DB 241 LCNARCNIMGPNYPIHSAKESQKGAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEWA 300
QY 301 RMLLRGCNVNSTSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRGCNVNSTSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDPGETPTFLASKIGRQLOQLMHI SRARKPAFILGSMRDEK 420
DB 361 DNVEIMKALIVFGAEVDTNDPGETPTFLASKIGRQLOQLMHI SRARKPAFILGSMRDEK 420
QY 421 RTHDHLCLDGGVKGGLIIIIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHLSKSM 480
DB 421 RTHDHLCLDGGVKGGLIIIIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHLSKSM 480
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DB 481 AYMRGMVFRMKDEVFGRSGRPYSGPLEEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPA 540
QY 541 ELHLFRNYDAPETVREPRFNQVNNLRPPAQPDSQLVWRAARSSGAAPTFRPNRFLDGG 600
DB 541 ELHLFRNYDAPETVREPRFNQVNNLRPPAQPDSQLVWRAARSSGAAPTFRPNRFLDGG 600
QY 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIIVSLGTRSPQVPTCDVFRPSNP 660
DB 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIIVSLGTRSPQVPTCDVFRPSNP 660
QY 661 WELAKTVFGAKELGKMWVDDCCTDDPGRP 688
DB 661 WELAKTVFGAKELGKMWVDDCCTDDPGRP 688

RESULT 3

US-09-927-180-23
; Sequence 23, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:08:24 ; Search time 25.3702 Seconds
(without alignments)
2024.365 Million cell updates/sec

Title: US-10-612-668-23

Perfect score: 3625

Sequence: 1 MQFFGRLVNTFSGVTNLFN.....GAKELGKVVVDCCTDPGRP 688

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
 - 2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
 - 3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
 - 4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
 - 6: /cgn2_6/ptodata/1/iaa/backfilees1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3625	100.0	688	2	US-08-555-568B-23
2	3625	100.0	688	3	US-09-519-223-23
3	3625	100.0	688	4	US-09-519-223-23
4	3606.5	99.5	687	2	US-08-555-568B-21
5	3606.5	99.5	687	3	US-09-519-223-21
6	3606.5	99.5	687	4	US-09-519-223-21
7	3572	98.5	819	4	US-09-949-016-10948
8	3315	91.4	752	1	US-08-281-193-2
9	3315	91.4	752	1	US-08-422-106-2
10	3315	91.4	752	2	US-08-735-716-2
11	3315	91.4	752	2	US-08-555-568B-2
12	3315	91.4	752	3	US-09-519-223-2
13	3315	91.4	752	4	US-09-927-180-2
14	3315	91.4	752	5	PCT-US95-08069-2
15	2084	57.5	394	2	US-08-555-568B-17
16	2084	57.5	394	3	US-09-519-223-17
17	2084	57.5	394	4	US-09-519-223-17
18	1531	42.2	292	2	US-08-555-568B-19
19	1531	42.2	292	3	US-09-519-223-19
20	1531	42.2	292	4	US-09-519-223-19
21	1165	32.1	896	4	US-09-270-767-46130
22	904	24.9	545	4	US-09-270-767-61684
23	371	10.2	143	4	US-09-270-767-33298
24	338	9.3	843	2	US-09-172-977-3
25	338	9.3	843	4	US-09-404-108-3
26	332	9.2	1839	2	US-09-172-977-4
27	332	9.2	1839	4	US-09-404-108-4

28	332	9.2	2753	4	US-09-949-016-7659	Sequence 7659, Ap
29	332	9.2	2753	4	US-09-949-016-7660	Sequence 7660, Ap
30	332	9.2	3924	4	US-09-538-092-1246	Sequence 1246, Ap
31	308.5	8.5	1745	2	US-09-031-485-33	Sequence 33, Appl
32	308.5	8.5	1745	2	US-08-847-429A-33	Sequence 33, Appl
33	308.5	8.5	1745	3	US-09-065-474-33	Sequence 33, Appl
34	308.5	8.5	1745	3	US-09-557-034-33	Sequence 33, Appl
35	301.5	8.3	786	4	US-09-509-802-2	Sequence 2, Appli
36	301.5	8.3	787	3	US-09-188-930-334	Sequence 334, App
37	301.5	8.3	787	4	US-09-312-283C-334	Sequence 334, App
38	296	8.2	1088	3	US-09-082-059-2	Sequence 2, Appli
39	296	8.2	3913	4	US-09-949-016-10933	Sequence 10933, A
40	296	8.2	4377	4	US-09-949-016-6978	Sequence 6978, Ap
41	294	8.1	1719	4	US-09-949-016-6966	Sequence 6966, Ap
42	294	8.1	1856	4	US-09-949-016-6964	Sequence 6964, Ap
43	294	8.1	1880	4	US-09-949-016-5876	Sequence 5876, Ap
44	294	8.1	1881	4	US-09-949-016-6965	Sequence 6965, Ap
45	294	8.1	1883	4	US-09-949-016-9010	Sequence 9010, Ap

ALIGNMENTS

RESULT 1
US-08-555-568B-23
; Sequence 23, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS: 25
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-23

Query Match 100.0%; Score 3625; DB 2; Length 688;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 688; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MQFFGRLVNTFSGVTNLFNPNFRKVEAVADYTSDDRVREGQLILFQNTPNRTDVCVLV	60
QY	61	NPRNSQSGFRLFOLELEADALVNFHYQSOLLFPYESSQVLTHTVQLHTDLIRNHPSW	120
Db	61	NPRNSQSGFRLFOLELEADALVNFHYQSOLLFPYESSQVLTHTVQLHTDLIRNHPSW	120

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; Publication No. US2003010482A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corp.
; APPLICANT: Bird, Timothy
; APPLICANT: Virca, G.D.
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS
; TITLE OF INVENTION: (DAKAR)
; FILE REFERENCE: 2889-US
; CURRENT APPLICATION NUMBER: US/10/299,327
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US/09/509,802
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-299-327-2

Query Match      8.3%; Score 301.5; DB 14; Length 786;
Best Local Similarity 29.1%; Pred. No. 2e-18;
Matches 95; Conservative 60; Mismatches 124; Indels 47; Gaps 12;

QY 112 DLIRNHPWSVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLAC-RKGDGEILVE 170
DB 434 DLVLD-SSASLLHLAVEAGQEECVKWLNNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
QY 171 LVQYCHTQMDVTDYKGETVFHYAVQ-GDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQ 229
DB 491 LLARKTSVNAKDEQDWTALHFAAQNGDEASTLLEKN--ASVNEVDEGRTPMHVACQ 548
QY 230 LGQEMVRVLLCNARCNIMGNGY-PIHSAMKFSQKCAEMI-----ISMDSQIHSKD 283
DB 549 HGOENIVRTLRRGVGVGLQGDAMLPVLYAAWQGLPIVKKLAKQPGVSVNAQTLDGRT 608
QY 284 PRYGA-----SPLHWAK---NAEMARMLLKRCGNVNST 313
DB 609 PLHLAAQRGHYRVARILDLCSVDNVCISLQAOPTPLHVAETGHTSTARLLHLRGAGEAL 668
QY 314 SSAGNTALHVGVMNRNRFDCAIVLLTHGANADARGHGNTPLHLAMSKDNVEMIKALIVFG 373
DB 669 TSEGYTALHAAQNGHLATVKLLIEEKADVMARGPLNQTLALHAAARGHSEVVEELV--S 726
QY 374 AE-VDPNDFGETPTFLASKIGRQLQ 398
DB 727 ADLIDLSDQGLSALHLAAQ-GRHSQ 751

RESULT 14
US-10-128-174-13
; Sequence 13, Application US/10128174
; Publication No. US20030199462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 31
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-128-174-31

Query Match      8.3%; Score 301.5; DB 14; Length 786;
Best Local Similarity 29.1%; Pred. No. 2e-18;
Matches 95; Conservative 60; Mismatches 124; Indels 47; Gaps 12;

QY 112 DLIRNHPWSVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLAC-RKGDGEILVE 170
DB 434 DLVLD-SSASLLHLAVEAGQEECVKWLNNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
QY 171 LVQYCHTQMDVTDYKGETVFHYAVQ-GDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQ 229
DB 491 LLARKTSVNAKDEQDWTALHFAAQNGDEASTLLEKN--ASVNEVDEGRTPMHVACQ 548
QY 230 LGQEMVRVLLCNARCNIMGNGY-PIHSAMKFSQKCAEMI-----ISMDSQIHSKD 283
DB 549 HGOENIVRTLRRGVGVGLQGDAMLPVLYAAWQGLPIVKKLAKQPGVSVNAQTLDGRT 608
QY 284 PRYGA-----SPLHWAK---NAEMARMLLKRCGNVNST 313
DB 609 PLHLAAQRGHYRVARILDLCSVDNVCISLQAOPTPLHVAETGHTSTARLLHLRGAGEAL 668
QY 314 SSAGNTALHVGVMNRNRFDCAIVLLTHGANADARGHGNTPLHLAMSKDNVEMIKALIVFG 373
DB 669 TSEGYTALHAAQNGHLATVKLLIEEKADVMARGPLNQTLALHAAARGHSEVVEELV--S 726
QY 374 AE-VDPNDFGETPTFLASKIGRQLQ 398
DB 727 ADLIDLSDQGLSALHLAAQ-GRHSQ 751

RESULT 15
US-10-128-174-31
; Sequence 31, Application US/10128174
; Publication No. US20030199462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 31
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-128-174-31

Query Match      8.3%; Score 301.5; DB 14; Length 786;
Best Local Similarity 29.1%; Pred. No. 2e-18;
Matches 95; Conservative 60; Mismatches 124; Indels 47; Gaps 12;

QY 112 DLIRNHPWSVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLAC-RKGDGEILVE 170
DB 434 DLVLD-SSASLLHLAVEAGQEECVKWLNNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
QY 171 LVQYCHTQMDVTDYKGETVFHYAVQ-GDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQ 229
DB 491 LLARKTSVNAKDEQDWTALHFAAQNGDEASTLLEKN--ASVNEVDEGRTPMHVACQ 548
QY 230 LGQEMVRVLLCNARCNIMGNGY-PIHSAMKFSQKCAEMI-----ISMDSQIHSKD 283
DB 549 HGOENIVRTLRRGVGVGLQGDAMLPVLYAAWQGLPIVKKLAKQPGVSVNAQTLDGRT 608
QY 284 PRYGA-----SPLHWAK---NAEMARMLLKRCGNVNST 313
DB 609 PLHLAAQRGHYRVARILDLCSVDNVCISLQAOPTPLHVAETGHTSTARLLHLRGAGEAL 668
QY 314 SSAGNTALHVGVMNRNRFDCAIVLLTHGANADARGHGNTPLHLAMSKDNVEMIKALIVFG 373
DB 669 TSEGYTALHAAQNGHLATVKLLIEEKADVMARGPLNQTLALHAAARGHSEVVEELV--S 726
QY 374 AE-VDPNDFGETPTFLASKIGRQLQ 398
DB 727 ADLIDLSDQGLSALHLAAQ-GRHSQ 751

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Db	529	--LEAGAAHSLATKGGTTPHLVAAKYGSLDVAKLLQORAAADSAGKNGLTPLHVAHYD	586
Qy	329	RFDCAIVLLTHGANADARGHGNTPHLHAMSKNVEMIKALIVFGAEDVTPNDPFGETPTF	388
Db	587	NQKVALLLEKGSAPHATAKNGYTPHLIAAKKNQWQIASTLLNYGAETNIVTKQGVTPPLH	646
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; Sequence 2, Application US/10164080			
; Publication No. US20030087411A1			
; GENERAL INFORMATION:			
; APPLICANT: BIRD, Timothy, A.			
; APPLICANT: HOLLAND, Pamela, M.			
; APPLICANT: PESCHON, Jacques, J.			
; APPLICANT: VIRCA, George, D.			
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS (DAK)			
; FILE REFERENCE: 3280-B			
; CURRENT APPLICATION NUMBER: US/10/164,080			
; PRIOR FILING DATE: 2002-06-04			
; PRIOR FILING DATE: 2001-06-04			
; PRIOR APPLICATION NUMBER: 60/334,362			
; PRIOR FILING DATE: 2001-11-29			
; NUMBER OF SEQ ID NOS: 7			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 2			
; LENGTH: 786			
; TYPE: PRT			
; ORGANISM: Mus sp.			
US-10-164-080-2			
Query Match 8.3%; Score 301.5; DB 14; Length 786;			
Best Local Similarity 29.1%; Pred. No. 2e-18;			
Matches 95; Conservative 60; Mismatches 124; Indels 47; Gaps 12			
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Db	434	DLVLD-SSASLLHLAVESQEECVKWLNNANPNLTNRKGSTPLHMAVERKGRG--IVE	490
Qy	171	LVQYCHTQMDVTDYKGTVTVEHYAVQ-GDNSQVOLLGRNAVAGLNQVNNQGLTPLHLACQ	229
Db	491	LLLRKTSVNAKEDQWTALHFAQNGDEASTRLLEKN--ASVNEVDFEGTTPHVAQCQ	548
Qy	230	LQKQEWYRVLLLCNARNINPGNGY-PHISAMKFSQKCAEMI-----ISMDSOQIHSKD	283
Db	549	HQGENIVRTLRRGVDVGLQKDAWPLHYAAWQGHLPVVKLLAQPGVSVNAQTLDGRT	608
Qy	284	PRVCA-----SPLHWAK---NAEMARMLLKRCNNVNST	313
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Db	669	TSGGYTALHAAQNGHLATVKLLIEEKADVWARGPLNQTLHLAAARGHSEVVEELV--S	726
Qy	374	AE-VDPNDFGETPTFLASKIGROLQ	398
Db	727	ADLIDLSDQGLSALHLAAQ-GRHSQ	751
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; Sequence 2, Application US/10299327			

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QY 207 RNAVAGLNQVNOGTLPLHLACQLGQKQEMVRVLLLCNARCNIIMGPNG-----Y 254
DB 375 KCCETMIQNTDSNGYTPAVA-----LINACLSNCQTLRGFGGQIQQSDSTQMAN 424
QY 255 PIHSAMKFSQ--KGCAEMIISMDSQIHSKDPYRGASPLHLAKNAEMARMMLKR---GCN 309
DB 425 PIIGAMKRGKLDVSLRKMLELKQDGLTETPTTGNVTIHCAINKKCLILLMEKFRDQTD 484
QY 310 VNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKAL 369
DB 485 PEARNALQOTPLHTFVKIDELGLVMTLSAYGVMDAQDINGNTPLHCAVTRGNTIARM 544
QY 370 IVFGAEVDPNDPGTPTFLASKI-----LLCLDGGGVKGLIIIIOLLIIEKASGVATKDL 457
DB 665 FPHEALRVRNKLKELVEKKTSNVINVLGDDGGIRGLVTQVQLICLAEFLDRPLIDY 724
QY 458 FDWAGTSTGGILALAILHSKSMAYMRGMYPFMKDEVFGRG-SRPYESGPLEEFLKREFGE 516
DB 725 FDMIGATSGCYIMSTMNTGSLRKAQRYLLFMKQOLFSDSWTRPYDTKTLETFIQAFGA 784
QY 517 HTKMTDVRKPKVMTLGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQIV 576
DB 785 DRLMGDIKYPFFCTTVRADTFPVQLELLRNRYLPISKE---NNDLGF---TDPNELTI 838
QY 577 WRAARSSGAAPTYFRPN-GRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSI 635
DB 839 WKATRRSSAAPTYSASEGKFIDGGMISNNPVLDMSDIGFYNTTCQKMRIPERKVMVMGC 898
QY 636 VVSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 688
DB 899 VLSVGTGITPCPVD-PSVFEMNDLFGMLR---GMKNLSLVVIDQATATGAP 947

RESULT 9
US-10-369-493-6690
; Sequence 6690, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6690
; LENGTH: 1023
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6690
Query Match 17.3%; Score 627; DB 15; Length 1023;
Best Local Similarity 23.9%; Pred. No. 1.5e-48;
Matches 195; Conservative 153; Mismatches 285; Indels 150; Gaps 23;
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QY 37 RVREBQILILFQNTNRTWDCVILVNPRNSQSGFRFLQLELEAD--ALVNFHOYSQQLPFF 94
DB 204 RAKEEEL---KNKELYHLAITLYNENNEKYVMSLFRSHKLDVVALCERCENPELPRV 260
QY 95 YESSPOV---LHTEVLQHLTDLIRNHPWSVAHLAVELGIRECFPH---SRIISCANCAE 148
DB 261 PPKVNIKDYLHT-----IFHELDRNMTWKSVHISSKIGLLEYFENMEKHLKYYLNLIV 315
QY 149 NREGTPLHLACRKGDEILVELVOYCHTQMDVDYKGETVHYAVQDGNOSVOLQL--G 206
DB 316 OPEGLSPLMIAVQNTQIETVSMMLDH-GADINILSSEQNVHLVAATASSGDLIKILWET 374
QY 207 RNAVAGLNQVNOGTLPLHLACQLGQKQEMVRVLLLCNARCNIIMGPNG-----Y 254
DB 375 KCCETMIQNTDSNGYTPAVA-----LINACLSNCQTLRGFGGQIQQSDSTQMAN 424
QY 255 PIHSAMKFSQ--KGCAEMIISMDSQIHSKDPYRGASPLHLAKNAEMARMMLKR---GCN 309
DB 425 PIIGAMKRGKLDVSLRKMLELKQDGLTETPTTGNVTIHCAINKKCLILLMEKFRDQTD 484
QY 310 VNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKAL 369
DB 485 PEARNALQOTPLHTFVKIDELGLVMTLSAYGVMDAQDINGNTPLHCAVTRGNTIARM 544
QY 370 IVFGAEVDPNDPGTPTFLASKI-----LLCLDGGGVKGLIIIIOLLIIEKASGVATKDL 457
DB 665 FPHEALRVRNKLKELVEKKTSNVINVLGDDGGIRGLVTQVQLICLAEFLDRPLIDY 724
QY 458 FDWAGTSTGGILALAILHSKSMAYMRGMYPFMKDEVFGRG-SRPYESGPLEEFLKREFGE 516
DB 725 FDMIGATSGCYIMSTMNTGSLRKAQRYLLFMKQOLFSDSWTRPYDTKTLETFIQAFGA 784
QY 517 HTKMTDVRKPKVMTLGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQIV 576
DB 785 DRLMGDIKYPFFCTTVRADTFPVQLELLRNRYLPISKE---NNDLGF---TDPNELTI 838
QY 577 WRAARSSGAAPTYFRPN-GRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSI 635
DB 839 WKATRRSSAAPTYSASEGKFIDGGMISNNPVLDMSDIGFYNTTCQKMRIPERKVMVMGC 898
QY 636 VVSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 688
DB 899 VLSVGTGITPCPVD-PSVFEMNDLFGMLR---GMKNLSLVVIDQATATGAP 947

RESULT 10
US-10-369-493-4998
; Sequence 4998, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4998
; LENGTH: 468
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Db 102 LCNARCNIMGNGYPIYSAMKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 161
QY 301 RMLLRKGCNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGNTPHLAMSK 360
Db 162 RMLLRKGCNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGNTPHLAMSK 221
QY 361 DNVEIMKALIVFGAEVDTNDGFTPTFLASKIGR-----OLQDLMIHSRARKPAFTLGSMDRDEKTHDL 426
Db 222 DNVEIMKALIVFGAEVDTNDGFTPTFLASKIGR-----OLQDLMIHSRARKPAFTLGSMDRDEKTHDL 281
QY 396 -----OLQDLMIHSRARKPAFTLGSMDRDEKTHDL 426
Db 282 VPAEQSSAHPHPSLERAQPPISLNNLEQLDLMIHSRARKPAFTLGSMDRDEKTHDL 341
QY 427 LCLDGGVGLIIIIQLLIAEKASGVATKDLFDWVAGTSTGGILALILHSKSMAYMRGM 486
Db 342 LCLDGGVGLIIIIQLLIAEKASGVATKDLFDWVAGTSTGGILALILHSKSMAYMRGM 401
QY 487 YFRMKDEVPRGSRPYESGLEFLKREGEHTKMTDVRKPKVMTGTTLSDRQPAELHLFR 546
Db 402 YFRMKDEVPRGSRPYESGLEFLKREGEHTKMTDVRKPKVMTGTTLSDRQPAELHLFR 461
QY 547 NYDAPETVREPFRNQVNLPRPAQPSDQLVWRAARSSGAAPYFRPNRGFLDGGILLANP 606
Db 462 NYDAPETVREPFRNQVNLPRPAQPSDQLVWRAARSSGAAPYFRPNRGFLDGGILLANP 521
QY 607 TLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPNPNWELAKT 666
Db 522 TLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPNPNWELAKT 581
QY 667 VFGAKELGMVYDCCDDPGR 687
Db 582 VFGAKELGMVYDCCDDPGR 602

RESULT 5
US-09-927-180-17
; Sequence 17, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-927-180-17
Query Match 57.5%; Score 2084; DB 9; Length 394;
Best Local Similarity 100.0%; Pred. No. 7.4e-185; Indels 0; Gaps 0;
Matches 394; Conservative 0; Mismatches 0;
QY 1 MQFFGRLVNTFSGVNTLFSNPFVRKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGRLVNTFSGVNTLFSNPFVRKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLEADALVNFHQSQQLLPFYESSQVLHTVQLHTDLIRNHPSW 120
Db 61 NPNRSQSGFRLEADALVNFHQSQQLLPFYESSQVLHTVQLHTDLIRNHPSW 120
QY 121 SVAHLAVELGIRECPHHSRIISCANCAENEGCTPLHLACRKGDEIILVELVQYCHTQMD 180
Db 121 SVAHLAVELGIRECPHHSRIISCANCAENEGCTPLHLACRKGDEIILVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLIGRNAVAGLNQNNQGLTPLHLACQLGKQEMVRVLL 240
Db 181 VTDYKGETVFHYAVQGDNSQVLQLIGRNAVAGLNQNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIMGNGYPIHSAMKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNIMGNGYPIHSAMKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRKGCNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGNTPHLAMSK 360
Db 301 RMLLRKGCNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGNTPHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDGFTPTFLASKIG 394
Db 361 DNVEIMKALIVFGAEVDTNDGFTPTFLASKIG 394

RESULT 6
US-09-927-180-19
; Sequence 19, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:

QY	601	LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP	660	QY	241	LCNARCNTMGPNGYPIHSAKFSQKGCABMIISMDSQIHSKDPKRYGASPLHWAKNAEMA	300
Db	600	LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP	659	Db	241	LCNARCNTMGPNGPSGFIHTAMKFSQKGCABMIISMDSQIHSKDPKRYGASPLHWAKNAEMA	300
QY	661	WELAKTVFGAKELGKMWVDCCTDPDGRP	688	QY	301	RMLLRGCNVNSTSAGNTALHVGWNRPFDCAI VLLTHGANADARGEHNTPLHLAMSK	360
Db	660	WELAKTVFGAKELGKMWVDCCTDPDGRP	687	Db	301	RMLLRGCNDVSTSAAGNTALHVA VNRNRFDCVMVLLTYGANAGTGEHNTPLHLAISK	360
RESULT 3							
US-09-927-180-2							
; Sequence 2, Application US/09927180							
; Patent No. US20020106364A1							
; GENERAL INFORMATION:							
; APPLICANT: Jones, Simon							
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B							
; NUMBER OF SEQUENCES: 25							
; CORRESPONDENCE ADDRESS:							
; ADDRESSEE: Genetics Institute, Inc.							
; STREET: 87 CambridgePark Drive							
; CITY: Cambridge							
; STATE: Massachusetts							
; COUNTRY: U.S.A.							
; ZIP: 02140							
; COMPUTER READABLE FORM:							
; MEDIUM TYPE: Floppy disk							
; COMPUTER: IBM PC compatible							
; OPERATING SYSTEM: PC-DOS/MS-DOS							
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)							
; CURRENT APPLICATION DATA:							
; APPLICATION NUMBER: US/09/927,180							
; FILING DATE: 09-Aug-2001							
; CLASSIFICATION: <Unknown>							
; PRIOR APPLICATION DATA:							
; APPLICATION NUMBER: 09/519,223							
; FILING DATE: <Unknown>							
; ATTORNEY/AGENT INFORMATION:							
; NAME: Brown, Scott A.							
; REGISTRATION NUMBER: 32,724							
; TELECOMMUNICATION INFORMATION:							
; TELEPHONE: (617) 498-8224							
; TELEFAX: (617) 876-5851							
; INFORMATION FOR SEQ ID NO: 2:							
; SEQUENCE CHARACTERISTICS:							
; LENGTH: 752 amino acids							
; TYPE: amino acid							
; TOPOLOGY: linear							
; MOLECULE TYPE: protein							
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:							
US-09-927-180-2							
Query Match 91.4%; Score 3315; DB 9; Length 752;							
Best Local Similarity 90.4%; Pred. No. 5e-299;							
Matches 621; Conservative 32; Mismatches 34; Indels 0; Gaps 0;							
QY	1	MQFFGLVNTFSGVTNLFNSNPRFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV	60	QY	1	MQFFGLVNTFSGVTNLFNSNPRFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV	60
Db	1	MQFFGLVNTLSSVTNLFNSNPRFRVKEISVADYTSHERVREEGQLILFQNASNRTWDCILV	60	Db	1	MQFFGLVNTFSGVTNLFNSNPRFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV	60
QY	61	NPRNSQSGRFLFQLELEADALVNFHQYSSQLLPFYESSQVLHTEVLOHLTDLIRNHPSW	120	QY	61	NPRNSQSGRFLFQLELEADALVNFHQYSSQLLPFYESSQVLHTEVLOHLTDLIRNHPSW	120
Db	61	SPRNPHSGRFLFQLESEADALVNFQFSPFPFYESSQVLHVEVLOHLSDDLIRSHPSW	120	Db	61	YPRNSQSGRFLFQLELEADALVNFHQYSS-----	89
QY	121	SVAHLAVELGIRCFHHSRIISCANCAENEBCGCTPLHLACRKGDDGILVELVOYCHTQMD	180	QY	121	SVAHLAVELGIRCFHHSRIISCANCAENEBCGCTPLHLACRKGDDGILVELVOYCHTQMD	180
Db	121	VTYHLAVELGIRCFHHSRIISCANSTENEBCGCTPLHLACRKGDSILVELVOYCHAQMD	180	Db	90	-----	89
QY	181	VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL	240	QY	181	VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL	240
Db	181	VTNKGETAHYAVQGDNSQVQLLQKNASAGLNQVNNKQGLTPLHLACQMGKQEMVRVLL	240	Db	90	-----QUGKQEMVRVLL	101
QY	241	LCNARCNTMGPNGYPIHSAKFSQKGCABMIISMDSQIHSKDPKRYGASPLHWAKNAEMA	300	QY	241	LCNARCNTMGPNGYPIHSAKFSQKGCABMIISMDSQIHSKDPKRYGASPLHWAKNAEMA	300
Db	241	VTNKGETAHYAVQGDNSQVQLLQKNASAGLNQVNNKQGLTPLHLACQMGKQEMVRVLL	240	Db	241	LCNARCNTMGPNGYPIHSAKFSQKGCABMIISMDSQIHSKDPKRYGASPLHWAKNAEMA	300

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; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-927-180-23

Query Match      100.0%; Score 3625; DB 9; Length 688;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 688; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQFFGLVNTFSGVNTLFSNPFVRKEVAVADYTSDDRVEEGQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGLVNTFSGVNTLFSNPFVRKEVAVADYTSDDRVEEGQLILFQNTPNRTWDCVLV 60

Qy 61 NPRNSQSGFRLFQLEADALVNFHOYSQQLLPFYESSQVLHTEVQLHTDLIRNHPSW 120
Db 61 NPRNSQSGFRLFQLEADALVNFHOYSQQLLPFYESSQVLHTEVQLHTDLIRNHPSW 120

Qy 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEIILVELVQYCHTQMD 180
Db 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEIILVELVQYCHTQMD 180

Qy 181 VTDYKGETVFHYAVOGDINSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDYKGETVFHYAVOGDINSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

Qy 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300

Qy 301 RMLLRKGCNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLRKGCNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360

Qy 361 DNVEIMKALIVFGAEVDTNDPFGTPTFLASKIGRQLODLMIHSRARKPAFTILGSMRDEK 420
Db 361 DNVEIMKALIVFGAEVDTNDPFGTPTFLASKIGRQLODLMIHSRARKPAFTILGSMRDEK 420

Qy 421 RTHDHLCLDGGVKGKLIILQIIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480
Db 421 RTHDHLCLDGGVKGKLIILQIIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480

Qy 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFKREFEHNTQMDVRKPKVMLTGLSDRQPA 540
Db 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFKREFEHNTQMDVRKPKVMLTGLSDRQPA 540

Qy 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRPNGRFLDGG 600
Db 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRPNGRFLDGG 600

STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match      99.5%; Score 3606.5; DB 9; Length 687;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MQFFGLVNTFSGVNTLFSNPFVRKEVAVADYTSDDRVEEGQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGLVNTFSGVNTLFSNPFVRKEVAVADYTSDDRVEEGQLILFQNTPNRTWDCVLV 60

Qy 61 NPRNSQSGFRLFQLEADALVNFHOYSQQLLPFYESSQVLHTEVQLHTDLIRNHPSW 120
Db 61 NPRNSQSGFRLFQLEADALVNFHOYSQQLLPFYESSQVLHTEVQLHTDLIRNHPSW 120

Qy 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEIILVELVQYCHTQMD 180
Db 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEIILVELVQYCHTQMD 180

Qy 181 VTDYKGETVFHYAVOGDINSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDYKGETVFHYAVOGDINSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

Qy 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300

Qy 301 RMLLRKGCNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLRKGCNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360

Qy 361 DNVEIMKALIVFGAEVDTNDPFGTPTFLASKIGRQLODLMIHSRARKPAFTILGSMRDEK 420
Db 361 DNVEIMKALIVFGAEVDTNDPFGTPTFLASKIGK-LQDLMIHSRARKPAFTILGSMRDEK 419

Qy 421 RTHDHLCLDGGVKGKLIILQIIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480
Db 420 RTHDHLCLDGGVKGKLIILQIIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 479

Qy 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFKREFEHNTQMDVRKPKVMLTGLSDRQPA 540
Db 480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFKREFEHNTQMDVRKPKVMLTGLSDRQPA 539

Qy 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRPNGRFLDGG 600
Db 540 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRPNGRFLDGG 599
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RESULT 2

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US-09-927-180-21
; Sequence 21, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TANG, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:20:02 ; Search time 93.803 Seconds
(without alignments)
2530.207 Million cell updates/sec

Title: US-10-612-668-23

Perfect score: 3625

Sequence: 1 MQGFLVNTFGVTLFSN.....GAKELGKVVVDCTDPDGRP 688

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 1462099

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications AA:*

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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3625	100.0	688	9 US-09-927-180-23	Sequence 23, Appl
2	3606.5	99.5	687	9 US-09-927-180-21	Sequence 21, Appl
3	3315	91.4	752	9 US-09-927-180-2	Sequence 2, Appl
4	2728.5	75.3	667	15 US-10-108-260A-3778	Sequence 3778, Ap
5	2084	57.5	394	9 US-09-927-180-17	Sequence 17, Appl
6	1531	42.2	292	9 US-09-927-180-19	Sequence 19, Appl
7	651	18.0	1071	15 US-10-369-493-6865	Sequence 6865, Ap
8	627	17.3	1023	15 US-10-369-493-6689	Sequence 6689, Ap
9	627	17.3	1023	15 US-10-369-493-6690	Sequence 6690, Ap
10	326	9.0	468	15 US-10-369-493-4998	Sequence 4998, Ap
11	324	8.9	1330	15 US-10-108-260A-3237	Sequence 3237, Ap
12	301.5	8.3	786	14 US-10-164-080-2	Sequence 2, Appl
13	301.5	8.3	786	14 US-10-299-327-2	Sequence 2, Appl

14	301.5	8.3	786	14	US-10-128-174-13	Sequence 13, Appl
15	301.5	8.3	786	14	US-10-128-174-31	Sequence 31, Appl
16	301.5	8.3	786	14	US-10-128-174-32	Sequence 32, Appl
17	301.5	8.3	786	14	US-10-128-174-33	Sequence 33, Appl
18	301.5	8.3	787	10	US-09-866-050A-334	Sequence 334, App
19	301.5	8.3	1724	9	US-09-964-899-43	Sequence 43, Appl
20	301	8.3	347	14	US-10-128-174-30	Sequence 30, Appl
21	296	8.2	1094	17	US-10-479-764-22	Sequence 22, Appl
22	296	8.2	3913	15	US-10-334-143-45	Sequence 45, Appl
23	293.5	8.1	1762	14	US-10-205-194-117	Sequence 117, App
24	286.5	7.9	720	15	US-10-433-794-20	Sequence 20, Appl
25	286.5	7.9	765	14	US-10-128-174-3	Sequence 3, Appl
26	286.5	7.9	765	14	US-10-128-174-34	Sequence 34, Appl
27	286.5	7.9	765	14	US-10-128-174-35	Sequence 35, Appl
28	286.5	7.9	765	14	US-10-128-174-36	Sequence 36, Appl
29	286.5	7.9	765	14	US-10-128-174-37	Sequence 37, Appl
30	286.5	7.9	765	14	US-10-128-174-38	Sequence 38, Appl
31	286.5	7.9	765	14	US-10-128-174-39	Sequence 39, Appl
32	286.5	7.9	765	14	US-10-128-174-40	Sequence 40, Appl
33	286.5	7.9	765	14	US-10-128-174-41	Sequence 41, Appl
34	286.5	7.9	765	14	US-10-128-174-42	Sequence 42, Appl
35	286.5	7.9	765	14	US-10-128-174-43	Sequence 43, Appl
36	286.5	7.9	765	14	US-10-128-174-44	Sequence 44, Appl
37	286.5	7.9	765	15	US-10-164-080-7	Sequence 56, Appl
38	284	7.8	784	14	US-10-164-080-7	Sequence 7, Appl
39	284	7.8	784	15	US-10-258-951-70	Sequence 70, Appl
40	282	7.8	784	14	US-10-354-358-38	Sequence 38, Appl
41	282	7.8	784	14	US-10-128-174-12	Sequence 12, Appl
42	282	7.8	784	15	US-10-658-904-2	Sequence 2, Appl
43	281	7.8	784	16	US-10-648-593-153	Sequence 153, App
44	273	7.5	367	15	US-10-250-613-6	Sequence 6, Appl
45	273	7.5	994	17	US-10-717-665-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1

US-09-927-180-23
; Sequence 23, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:

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Qy	601	LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIIVSLGTGRSPQVPVTCVDVFRPSNP	660
Db	601	LLANNPTLDAMTEIHEYNQDMIRKQGNKVKKLSIIVSLGTGRSPQVPVTCVDVFRPSNP	660
Qy	661	WELAKTVFGAKELGKMVDDCCTDPDGR	687
Db	661	WELAKTVFGAKELGKMVDDCCTDPDGR	687

Search completed: May 26, 2005, 14:13:57
Job time : 92.0457 secs

Db 121 TVTHLAVELGIRECFHSHSRIISCANSTENEEGCTPLHLACRGKDSSEILVELVQYCHAQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGQKQEMVRVLL 240
Db 181 VTDNKGETAFAHYAVQGDNSQVLLGKNASAGLNQVNNQGLTPLHLACQMGQEMVRVLL 240
QY 241 LCNARCNIMGPNYPIHSAKFSQKCAEMIIISMDSSQIHSKDPYKASPLHAKNAEMA 300
Db 241 LCNARCNVMGSPGFIHTAMKFSQKCAEMIIISMDSSQIHSKDPYKASPLHAKNAEMA 300
QY 301 RMLLRKGCNVNSTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLRKGCNDVSTSAAGNTALHVAVMNRFDCAIIVLLTHGANAGTGEHNTPLHLAISK 360
QY 361 DNVMEMIKALIVFGAEVDTFNDGETPTFLASKIGRQLQDLMIHSRARKPAFILGSRDEK 420
Db 361 DNVMEMIKALIVFGAEVDTFNDGETPTFAFASKISQQLQDLMIHSRARKPAFILGSRDEK 420
QY 421 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGILAILHLSKSM 480
Db 421 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGILAILHLSKSM 480
QY 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEEFKREFEGHTKMTDVRKPKVMTLGTLSDRQPA 540
Db 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEEFKREFEGHTKMTDVRKPKVMTLGTLSDRQPA 540
QY 541 ELHLFRNYDAPETVREPRNQVNNLRPPAQPSDQVWRAARSSGAAPTFRPGRFLDGG 600
Db 541 ELHLFRNYDAPETVREPRNQVNNLRPPAQPSDQVWRAARSSGAAPTFRPGRFLDGG 600
QY 601 LIANPTLDAMTEIHEYNODLIRKGOANKVKLSIIVSLGTGRSPQVPTCVDFRPSNP 660
Db 601 LIANPTLDAMTEIHEYNODLIRKGOANKVKLSIIVSLGTGRSPQVPTCVDFRPSNP 660
QY 661 WELAKTVFGAKELGKMWVDDCTDPDGR 687
Db 661 WELAKTVFGAKELGKMWVDDCTDPDGR 687

RESULT 15
ABB82215
ID ABB82215 standard; protein; 752 AA.
XX AC ABB82215;
XX DT 08-JAN-2003 (first entry)
XX DE Calcium independent phospholipase A2/B (cPLA2/B) (clone 9).
XX KW Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
XX KW antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;
XX OS Unidentified.
XX PN US2002106364-A1.
XX PD 08-AUG-2002.
XX PF 09-AUG-2001; 2001US-00927180.
XX PR 27-JUL-1994; 94US-00281193.
XX PR 14-APR-1995; 95US-00422106.
XX PR 14-APR-1995; 95US-00422420.
XX PR 26-JUN-1995; 95WO-05008069.
XX PR 08-NOV-1995; 95US-00555568.
XX PR 09-SEP-1998; 98US-00149988.
XX PR 06-MAR-2000; 2000US-00519223.
XX (GEM) GENETICS INST INC.
XX PA Jones S, Tang J;
XX PI
XX

WPI: 2002-739923/80.
N-PSDB; ABV73007.
Novel composition comprising purified mammalian calcium independent phospholipase enzyme, useful for the screening of inhibitors of phospholipase activity, is active in the absence of calcium.
Example 4; Page 10-12; 41pp; English.
The invention relates to a purified mammalian calcium independent cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is characterized by activity in the absence of calcium and has a molecular weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified calcium independent phospholipase enzyme is useful for identifying an inhibitor of phospholipase activity which involves combining (I), phospholipid and candidate inhibitor compound, and observing whether the enzyme cleaves the phospholipid and releases fatty acid from it. A pharmaceutical composition (PC) comprising a therapeutically effective amount of the inhibitor is useful for reducing inflammation and for treating inflammatory conditions including rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease and other diseases mediated by increased levels of prostaglandins, leukotriene or platelet activating factor. A composition comprising an antibody which binds to (I) is useful as research and diagnostic tool, and is also useful in the study of phospholipase A2 activity and inflammatory conditions. The present sequence represents a cPLA2/B enzyme (clone 9)
Sequence 752 AA;
Query Match 91.4%; Score 3315; DB 5; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 32; Mismatches 34; Indels 0; Gaps 0;
QY 1 MQFFGLVNTSGVTNLFNSNPRVKEVAVADYTSSDRVEEGQLILFQNTNRTWDCVILV 60
Db 1 MQFFGLVNTLSSVTNLFNSNPRVKEISVADYTSHERVREEGQLILFQNASRNTWDCILV 60
QY 61 NPNRSGQFRLEADALVNFHQSOLLPPFYESSPOVLTEVQLHQLTLIRHPSW 120
Db 61 SPNPHSGFRLEADALVNFQFSQSPFYESSQVFLHVEVLQHLISLRHPSW 120
QY 121 SVAHLAVELGIRECFHSHSRIISCANCAENEECTPLHLACRGKDSSEILVELVQYCHTQMD 180
Db 121 TVTHLAVELGIRECFHSHSRIISCANSTENEECTPLHLACRGKDSSEILVELVQYCHAQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGQKQEMVRVLL 240
Db 181 VTDNKGETAFAHYAVQGDNSQVLLGKNASAGLNQVNNQGLTPLHLACQMGQEMVRVLL 240
QY 241 LCNARCNIMGPNYPIHSAKFSQKCAEMIIISMDSSQIHSKDPYKASPLHAKNAEMA 300
Db 241 LCNARCNVMGSPGFIHTAMKFSQKCAEMIIISMDSSQIHSKDPYKASPLHAKNAEMA 300
QY 301 RMLLRKGCNVNSTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLRKGCNDVSTSAAGNTALHVAVMNRFDCAIIVLLTHGANAGTGEHNTPLHLAISK 360
QY 361 DNVMEMIKALIVFGAEVDTFNDGETPTFLASKIGRQLQDLMIHSRARKPAFILGSRDEK 420
Db 361 DNVMEMIKALIVFGAEVDTFNDGETPTFAFASKISQQLQDLMIHSRARKPAFILGSRDEK 420
QY 421 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGILAILHLSKSM 480
Db 421 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGILAILHLSKSM 480
QY 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEEFKREFEGHTKMTDVRKPKVMTLGTLSDRQPA 540
Db 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEEFKREFEGHTKMTDVRKPKVMTLGTLSDRQPA 540
QY 541 ELHLFRNYDAPETVREPRNQVNNLRPPAQPSDQVWRAARSSGAAPTFRPGRFLDGG 600
Db 541 ELHLFRNYDAPETVREPRNQVNNLRPPAQPSDQVWRAARSSGAAPTFRPGRFLDGG 600

FH	Key	Location/Qualifiers	
FT	Active-site	465	
FT	/note= "mutagenesis of Ser-465 results in loss of activity"		
FT			
XX			
PN	WO9717448-A2.		
XX			
PD	15-MAY-1997.		
XX			
PF	07-NOV-1996;	96WO-US017794.	
XX			
PR	08-NOV-1995;	95US-00555568.	
XX			
PA	(GEMY) GENETICS INST INC.		
XX			
PI	Jones S, Tang J;		
XX			
DR	WPI; 1997-281037/25.		
DR	N-PSDB; AAT68827.		
XX			
PT	Calcium independent phospholipase A2/B - used to reduce inflammation in a mammalian subject.		
XX			
PS	Example 4; Page 33-36; 74pp; English.		
XX			
CC	A novel hamster cytosolic phospholipase A2/B (sPLA2/B) (AAW17849) is thought to be involved in the arachidonic acid cascade. Its amino acid sequence was deduced from a cDNA clone (AAT68827) obtd. from a CHO-DUX cDNA library. The recombinant enzyme has been expressed in CHO and COS host cells. Human sPLA2/B polypeptides (see also AAW17845-48) have also been isolated. These can be used to screen for inhibitors useful as antiinflammatory agents that block the arachidonic acid cascade in mammals. (Updated on 27-AUG-2003 to correct OS field.)		
XX			
SQ	Sequence 752 AA;		
Query Match 91.4%; Score 3315; DB 2; Length 752;			
Best Local Similarity 90.4%; Pred. No. 0;			
Matches 621; Conservative 32; Mismatches 34; Indels 0; Gaps 0;			
QY	1	MQFFGLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREGQLILFQNTPNRTWDCVLV 60	
DB	1	MQFFGLVNTLSSVTNLFNSNPRVKEISVADYTSHERVREGQLILFQNASNRTWDCILV 60	
QY	61	NPRNSOGRLFOLEADALVNFHOYSQOLLFPYESSPOVLHTEVLQHLTDLIRNHPWS 120	
DB	61	SPRNPSSGRLFOLESEADALVNFQFSQLPFFYESSQVVLHVEVLQHLSDILIRHPSW 120	
QY	121	SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 180	
DB	121	TVTHLAVELGIRECFHHSRIISCANSTENEEGCTPLHLACRKGDSIILVELVQYCHQMD 180	
QY	181	VTDTKETVPHYAVQDGNOSVOLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240	
DB	181	VTDNKETAFHYAVQDGNOSVOLQLGKNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240	
QY	241	LCNARCNIWGPNGYPIHSAKFSQKCAEMIISMDSSQIHSKDPYCASPLHWAKNAEMA 300	
DB	241	LCNARCNIWGPNGSFPPIHTAMKFSQKCAEMIISMDSSQIHSKDPYCASPLHWAKNAEMA 300	
QY	301	RMLLRKGCNVNSTSSAGNTALHVGVMNRFRDCAIVLLTHGANADARGEHNTPLHLAMSK 360	
DB	301	RMLLRKGCVDVSTSAAGNTALHVAVNRFRDCVMVLLTYGANAGTPEGHNTPLHLAISK 360	
QY	361	DNVEMIKALIVGAEDVTPNDFGETPTFLASKIGROLQDLMIHSRARKPAFILGSRMDEK 420	
DB	361	DNMEMIKALIVGAEDVTPNDFGETPAFMASKISKQLQDLMPISRARKPAFILSSRMDEK 420	
QY	421	RTHDHLCLDGGGVKGLIIQLLIAEKASGVATKOLFDMVAGTSGTGLALAILHKS 480	
DB	421	RIHDHLCLDGGGVKGLIIQLLIAEKASGVATKOLFDMVAGTSGTGLALAILHKS 480	
QY	481	AYMRGMYFRMKDEVFRGSRPYESGPLEEFLKRFEGEHTKMTDVRKPKWMLTGLTSLDRQPA 540	
DB	481	AYMRGYFRMKDEVFRGSRPYESGPLEEFLKRFEGEHTKMTDVKPKWMLTGLTSLDRQPA 540	
QY	541	ELHLFRNYDAPETVREPRFNQNVNLPAPQSPDQLVRAARSSGAAPTYPFRPNRGFLDGG 600	
DB	541	ELHLFRNYDAPETVREPRFNQNVNLPAPQSPDQLVRAARSSGAAPTYPFRPNRGFLDGG 600	
QY	601	LLANNPFLDAMTBIHEYNDQILIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660	
DB	601	LLANNPFLDAMTBIHEYNDQIRKQGNKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660	
QY	661	WELAKTVFGAKELGKMWVDCCTDPPDGR 687	
DB	661	WELAKTVFGAKELGKMWVDCCTDPPDGR 687	
RESULT 14			
AAW81825			
ID	AAW81825 standard; protein; 752 AA.		
XX			
AC	AAW81825;		
XX			
DT	02-FEB-1999 (first entry)		
XX			
DE	Chinese hamster calcium independent cPLA2/B protein.		
XX			
KW	Calcium independent; cytosolic phospholipase A2/B; cPLA2/B; screening; anti-inflammatory; arachidonic acid cascade; chinese hamster.		
XX			
OS	Cricetulus griseus.		
XX			
PN	US5840511-A.		
XX			
PD	24-NOV-1998.		
XX			
PF	23-OCT-1996; 96US-00735716.		
PR	27-JUL-1994; 94US-00281193.		
PR	14-APR-1995; 95US-00422106.		
XX			
PA	(GEMY) GENETICS INST INC.		
XX			
PI	Tang J, Jones S;		
XX			
DR	WPI; 1999-034032/03.		
DR	N-PSDB; AAV64840.		
XX			
PT	Screening assay for phospholipase inhibitors - using specified phospholipase polypeptide.		
XX			
PS	Claim 1b; Col 21-24; 24pp; English.		
XX			
CC	This sequence represents a novel calcium independent cytosolic phospholipase A2/B enzyme isolated from chinese hamster ovary cells. This protein can be used for screening unknown compounds for anti-inflammatory activity mediated by the arachidonic acid cascade		
XX			
SQ	Sequence 752 AA;		
Query Match 91.4%; Score 3315; DB 2; Length 752;			
Best Local Similarity 90.4%; Pred. No. 0;			
Matches 621; Conservative 32; Mismatches 34; Indels 0; Gaps 0;			
QY	1	MQFFGLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREGQLILFQNTPNRTWDCVLV 60	
DB	1	MQFFGLVNTLSSVTNLFNSNPRVKEISVADYTSHERVREGQLILFQNASNRTWDCILV 60	
QY	61	NPRNSOGRLFOLEADALVNFHOYSQOLLFPYESSPOVLHTEVLQHLTDLIRNHPWS 120	
DB	61	SPRNPSSGRLFOLESEADALVNFQFSQLPFFYESSQVVLHVEVLQHLSDILIRHPSW 120	
QY	121	SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 180	
DB	121	TVTHLAVELGIRECFHHSRIISCANSTENEEGCTPLHLACRKGDSIILVELVQYCHQMD 180	
QY	181	VTDTKETVPHYAVQDGNOSVOLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240	
DB	181	VTDNKETAFHYAVQDGNOSVOLQLGKNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240	
QY	241	LCNARCNIWGPNGYPIHSAKFSQKCAEMIISMDSSQIHSKDPYCASPLHWAKNAEMA 300	
DB	241	LCNARCNIWGPNGSFPPIHTAMKFSQKCAEMIISMDSSQIHSKDPYCASPLHWAKNAEMA 300	
QY	301	RMLLRKGCNVNSTSSAGNTALHVGVMNRFRDCAIVLLTHGANADARGEHNTPLHLAMSK 360	
DB	301	RMLLRKGCVDVSTSAAGNTALHVAVNRFRDCVMVLLTYGANAGTPEGHNTPLHLAISK 360	
QY	361	DNVEMIKALIVGAEDVTPNDFGETPTFLASKIGROLQDLMIHSRARKPAFILGSRMDEK 420	
DB	361	DNMEMIKALIVGAEDVTPNDFGETPAFMASKISKQLQDLMPISRARKPAFILSSRMDEK 420	
QY	421	RTHDHLCLDGGGVKGLIIQLLIAEKASGVATKOLFDMVAGTSGTGLALAILHKS 480	
DB	421	RIHDHLCLDGGGVKGLIIQLLIAEKASGVATKOLFDMVAGTSGTGLALAILHKS 480	
QY	481	AYMRGMYFRMKDEVFRGSRPYESGPLEEFLKRFEGEHTKMTDVRKPKWMLTGLTSLDRQPA 540	
DB	481	AYMRGYFRMKDEVFRGSRPYESGPLEEFLKRFEGEHTKMTDVKPKWMLTGLTSLDRQPA 540	
QY	541	ELHLFRNYDAPETVREPRFNQNVNLPAPQSPDQLVRAARSSGAAPTYPFRPNRGFLDGG 600	
DB	541	ELHLFRNYDAPETVREPRFNQNVNLPAPQSPDQLVRAARSSGAAPTYPFRPNRGFLDGG 600	
QY	601	LLANNPFLDAMTBIHEYNDQILIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660	
DB	601	LLANNPFLDAMTBIHEYNDQIRKQGNKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660	
QY	661	WELAKTVFGAKELGKMWVDCCTDPPDGR 687	
DB	661	WELAKTVFGAKELGKMWVDCCTDPPDGR 687	

Db 421 RIHDLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKM 480

Qy 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEBFLKREFGHEHTKMTDVRKPKVMTGLTSLDRQPA 540

Db 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEBFLKREFGHEHTKMTDVRKPKVMTGLTSLDRQPA 540

Qy 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRAARSSGAAPTYFRNGRFLDGG 600

Db 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRAARSSGAAPTYFRNGRFLDGG 600

Qy 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIWSLGTGRSPQVPVTCVDVFRPSNP 660

Db 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIWSLGTGRSPQVPVTCVDVFRPSNP 660

Qy 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

Db 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 12

AAW13163

ID AAW13163 standard; protein; 752 AA.

XX AC AAW13163;

XX 17-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 20-MAY-1997 (first entry)

XX Ca-independent phospholipase A2/B protein.

XX Ca-independent phospholipase A2/B; Chinese hamster ovary cell; probe;

KW chromatography; DEAE anion exchange; hydrophobic interaction; lambda;

KW heparin Toyopearl; chromatofocusing; eukaryotic expression vector; COS;

KW CHO; inhibitor; anti-inflammatory agent; arachidonic acid cascade.

XX Cricetulus griseus; ovary cells.

OS US5589170-A.

XX 31-DEC-1996.

PD 14-APR-1995; 95US-00422106.

XX 27-JUL-1994; 94US-00281193.

PR (GENY) GENETICS INST INC.

PA Tang J, Jones S;

PI WPI; 1997-076789/07.

XX N-PSDB; AAT59199.

DR Compens. comprising calcium-independent phospholipase enzyme - for

PT screening for anti-inflammatory agents.

XX Claim 5; Col 15-22; 24pp; English.

XX This is the amino acid sequence of the Ca-independent phospholipase A2/B

CC from Chinese hamster ovary cells. The protein was isolated from these

CC cells by conventional chromatographic methods e.g. DEAE anion exchange,

CC hydrophobic interaction, heparin Toyopearl and Mono P 5/20

CC chromatofocusing chromatography. The purified protein has mol. wt. of 86

CC kD and an optimum pH 6. The protein was used for amino acid sequencing

CC from which pools of degenerate probes were synthesised. The probes were

CC used to screen a CHO cell cDNA library in lambda ZAPII vector. Of 400000

CC recombinant phages screened, 12 positive plaques were isolated. One of

CC these, designated clone 9, contained this sequence. The phospholipase

CC gene can be inserted into eukaryotic vectors for expression in COS or CHO

CC cells. The protein, or peptides derived from it e.g. AAW13164-76, can be

CC used to identify phospholipase inhibitors that can be used as anti-

CC inflammatory agents, esp. against components of the arachidonic acid

CC cascade. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT

CC -2003 to standardise OS field)

XX Sequence 752 AA;

Qy Query Match 91.4%; Score 3315; DB 2; Length 752;

Best Local Similarity 90.4%; Pred. No. 0;

Matches 621; Conservative 32; Mismatches 34; Indels 0; Gaps 0;

Qy 1 MQFGRLVNTSGVTNLFSPNPRVKEVAVADYTSDDRVRREGQLILPONTNRTWDCVILV 60

Db 1 MQFGRLVNTLSSVTNLFSPNPRVKEISVADYTSHERVRREGQLILFQVNSNRTWDCVILV 60

Qy 61 NPNRSQSQRFLFOLELEADALVNFHOYSSQLLPFYESSPOVLHTVLOHLTLINHPSW 120

Db 61 SPRNPHSGRFLFOLESEADALVNFQPSQSPFFYESSVQVLHVLEVLOHLSLIRHPSW 120

Qy 121 SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEIILVELVQYCHTQMD 180

Db 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRKGDEIILVELVQYCHQMD 180

Qy 181 VTDYKGETVPHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGQKQEMVRVLL 240

Db 181 VTDNKGETAFFHYAVQGDNSQVLQLGKNASAGLNQVNRQGLTPLHLACQMGKQEMVRVLL 240

Qy 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSDKDPYRGASPLHWAQNAEMA 300

Db 241 LCNARCNVWGSPGPIHTAMKFSQKCAEMIISMDSSQIHSDKDPYRGASPLHWAQNAEMA 300

Qy 301 RMLLKRCNVNSTSAGNTALHVGVMNRNFDCAIYLLTHGANADARGHGNTPPLHLAMSK 360

Db 301 RMLLKRCGCDVSTSAAGNTALHVAVMNRNFDCAIYLLTHGANAGTPGEHGNTPPLHLAISK 360

Qy 361 DNEMIKALIYFGAEVDPNDFGETPFAWASKISKQLQDLMPISARKPAFTLSSMRDEK 420

Db 361 DNEMIKALIYFGAEVDPNDFGETPFAWASKISKQLQDLMPISARKPAFTLSSMRDEK 420

Qy 421 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKM 480

Db 421 RIHDLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKM 480

Qy 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEBFLKREFGHEHTKMTDVRKPKVMTGLTSLDRQPA 540

Db 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEBFLKREFGHEHTKMTDVRKPKVMTGLTSLDRQPA 540

Qy 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRAARSSGAAPTYFRNGRFLDGG 600

Db 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRAARSSGAAPTYFRNGRFLDGG 600

Qy 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIWSLGTGRSPQVPVTCVDVFRPSNP 660

Db 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIWSLGTGRSPQVPVTCVDVFRPSNP 660

Qy 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

Db 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 13

AAW17849

ID AAW17849 standard; protein; 752 AA.

XX AC AAW17849;

XX 27-AUG-2003 (revised)

DT 07-AUG-1997 (first entry)

XX Hamster cytosolic phospholipase A2/B.

XX Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;

KW inflammation; inhibitor; antiinflammatory; CHO.

XX Cricetus.

OS

QY 607 TLDAMTEIHEYNQDLIRKQANKVKKLSIVSLGTGRSPQVPVTCVDVFRPSNPWELAKT 666
DB |||||TLDAMTEIHEYNQDLIRKQANKVKKLSIVSLGTGRSPQVPVTCVDVFRPSNPWELAKT 720
QY 667 VFGAKELGKVVDCCTDPDGR 687
DB |||||VFGAKELGKVVDCCTDPDGR 741

RESULT 8
ABM84355
ID ABM84355 standard; protein; 810 AA.
AC AC
XX ABM84355;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4604.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
XX (INCY-) INCYTE CORP.
XX
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen P;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX WPI: 2004-329368/30.
DR N-PSDB; ACN43007.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 810 AA;

Query Match 98.3%; Score 3563; DB 8; Length 810;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 686; Conservative 0; Mismatches 1; Indels 58; Gaps 2;

QY 1 MQFFGRLVNTFSGVNLFNSNPRVKEVAVADVTSSDRVREEGQLILFQNTPNRTWDCVLV 60
DB |||||MQFFGRLVNTFSGVNLFNSNPRVKEVAVADVTSSDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLELEADALVNFHOYSQQLLPFYESSPQVLHTEVQLHLDLIRNHPSW 120
DB |||||NPNRSQSGFRLFQLELEADALVNFHOYSQQLLPFYESSPQVLHTEVQLHLDLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHHSRII-----SCANCAENE 152
DB |||||SVAHLAVELGIRECFHHSRIIIRVSAHQVPLGWLWELISTHETFEFSPPKSCANCAENE 180
QY 153 CTPHLACRKGDEILVELVQYCHTQMDVTDYKGETVFHYAVQGDNSQVQLLGRNAVAG 212
DB |||||CTPHLACRKGDEILVELVQYCHTQMDVTDYKGETVFHYAVQGDNSQVQLLGRNAVAG 240
QY 213 LNQVNNQGLTPLHLACQLGKQEMVRVLLLCNARCNTIMGPNGYPIHSAMKFSQKGCAMII 272
DB |||||LNQVNNQGLTPLHLACQLGKQEMVRVLLLCNARCNTIMGPNGYPIHSAMKFSQKGCAMII 300
QY 273 SMDSSQIHSKDPYRGASPLHWAQNAEMARMLLKRCNVNSTSSAGNTALHVGVMRNFDC 332
DB |||||SMDSSQIHSKDPYRGASPLHWAQNAEMARMLLKRCNVNSTSSAGNTALHVGVMRNFDC 360
QY 333 AIVLLTHGANADARGEHGNTPHLAMSKDNVEMIKALIVFGAEVDTNPDPGPTPTFLASK 392
DB |||||AIVLLTHGANADARGEHGNTPHLAMSKDNVEMIKALIVFGAEVDTNPDPGPTPTFLASK 420
QY 393 IGRQQLDLWHISRAKRPAPILGSMRDEKTHDHLCLDGGGVKGLIIQLLIAIERKASGV 452
DB |||||IGRQQLDLWHISRAKRPAPILGSMRDEKTHDHLCLDGGGVKGLIIQLLIAIERKASGV 480
QY 453 ATKDLFDWAGVSTGGILALAILHKSMAVMRGMTFRMKDEVFRGSRPYESGLEEFLLKR 512
DB |||||ATKDLFDWAGVSTGGILALAILHKSMAVMRGMTFRMKDEVFRGSRPYESGLEEFLLKR 540
QY 513 EFGHEKMTDVRKPK-----VMLTGTLSDRPAEL 542
DB |||||EFGHEKMTDVRKPKLDQSDTTPALPERACFAGMVRGEAHLSTRTEYMLTGTLSDRPAEL 600
QY 543 HLFNRYDAPETVREPRENQNVNLRPPAOPSDOLVWRAARSSGAAPYFRPNGRFLDGLL 602
DB |||||HLFNRYDAPETVREPRENQNVNLRPPAOPSDOLVWRAARSSGAAPYFRPNGRFLDGLL 650
QY 603 ANNPILDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNPWE 662
DB |||||ANNPILDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNPWE 720
QY 663 LAKTVFGAKELGKVVDCCTDPDGR 687
DB |||||LAKTVFGAKELGKVVDCCTDPDGR 745

RESULT 9
ABM84354
ID ABM84354 standard; protein; 810 AA.
XX
AC ABM84354;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4603.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX

Db 181 VTDYGETVFHYAVQDQNSQVQLLGRNAVAGLNVNNGQLTPLHLACQLGQKQWVRVLL 240
 Qy 241 LCNARCNIIMPNGYPIHSAKFSQKGAEMIISMDSSQIHSKDPYKASPLHWAKNAEMA 300
 Db 241 LCNARCNIIMPNGYPIHSAKFSQKGAEMIISMDSSQIHSKDPYKASPLHWAKNAEMA 300
 Qy 301 RMLLKGCCNVNSTSSAGNTALHVGWVRNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
 Db 301 RMLLKGCCNVNSTSSAGNTALHVGWVRNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
 Qy 361 DNVEIMKALIVFGAEVDTNDGFTPTFLASKIGR----- 395
 Db 361 DNVEIMKALIVFGAEVDTNDGFTPTFLASKIGRLVTRKAILTLRTVGAECYCPPIHG 420
 Qy 396 -----QLQDLMHISPAKPAFTLGSMRDEKTRTHDL 426
 Db 421 VPAEQGSAAPHHPFSLERAQPPISLNLELQDLMHISPAKPAFTLGSMRDEKTRTHDL 480
 Qy 427 LCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRGM 486
 Db 481 LCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRGM 540
 Qy 487 YFRMKDEVFRGSRPYESGPLEEFKKEFGHTKMTDVRKPKVMTGLTSDROPAPAEHLHFR 546
 Db 541 YFRMKDEVFRGSRPYESGPLEEFKKEFGHTKMTDVRKPKVMTGLTSDROPAPAEHLHFR 600
 Qy 547 NYDAPETVREPRFNQNVNLRPPAQSDQLVWRAARSSGAAPTYFRPNGRFLDGLLANNP 606
 Db 601 NYDAPETVREPRFNQNVNLRPPAQSDQLVWRAARSSGAAPTYFRPNGRFLDGLLANNP 660
 Qy 607 TLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDPFRPNWELAKT 666
 Db 661 TLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDPFRPNWELAKT 720
 Qy 667 VFGAKELGKVVDCCTDDPGR 687
 Db 721 VFGAKELGKVVDCCTDDPGR 741

RESULT 7
 ADO19776
 ID ADO19776 standard; protein; 806 AA.
 AC ADO19776;
 DT 12-AUG-2004 (first entry)
 DE Human PRO polypeptide #350.
 KW Human; PRO; immune related disorder; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KW diabetes mellitus; renal disease; demyelinating disease;
 KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.
 OS Homo sapiens.
 PN WO2004043361-A2.
 PD 27-MAY-2004.
 PF 06-NOV-2003; 2003WO-US035268.
 PR 08-NOV-2002; 2002US-0425235P.
 PA (GETH) GENENTECH INC.
 XX Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 PI Wood WI, Wu TD;

XX WPI; 2004-420067/39.
 DR N-PSDB; ADO19775.
 XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthritis.
 XX Claim 7; SEQ ID NO 700; 1731pp; English.
 XX The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polyneuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the
 CC invention.
 XX Sequence 806 AA;
 SQ
 Query Match 98.5%; Score 3572; DB 8; Length 806;
 Best Local Similarity 92.4%; Pred. No. 0;
 Matches 685; Conservative 1; Mismatches 1; Indels 54; Gaps 1;
 Qy 1 MOFFRLVNTSGVNTLFSNPRVKEVAVADYTSDDRVREEQQLILFQNTNRTWDCVILV 60
 Db 1 MOFFRLVNTSGVNTLFSNPRVKEVAVADYTSDDRVREEQQLILFQNTNRTWDCVILV 60
 Qy 61 NPNRSQSGFRLEADALVNFHOYSQQLPPFYESSQVLTHTVQLHTLIRNHPSW 120
 Db 61 NPNRSQSGFRLEADALVNFHOYSQQLPPFYESSQVLTHTVQLHTLIRNHPSW 120
 Qy 121 SVLAHVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEILVELVQYCHTQMD 180
 Db 121 SVLAHVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEILVELVQYCHTQMD 180
 Qy 181 VTDYGETVFHYAVQDQNSQVQLLGRNAVAGLNVNNGQLTPLHLACQLGQKQWVRVLL 240
 Db 181 VTDYGETVFHYAVQDQNSQVQLLGRNAVAGLNVNNGQLTPLHLACQLGQKQWVRVLL 240
 Qy 241 LCNARCNIIMPNGYPIHSAKFSQKGAEMIISMDSSQIHSKDPYKASPLHWAKNAEMA 300
 Db 241 LCNARCNIIMPNGYPIHSAKFSQKGAEMIISMDSSQIHSKDPYKASPLHWAKNAEMA 300
 Qy 301 RMLLKGCCNVNSTSSAGNTALHVGWVRNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
 Db 301 RMLLKGCCNVNSTSSAGNTALHVGWVRNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
 Qy 361 DNVEIMKALIVFGAEVDTNDGFTPTFLASKIGR----- 395
 Db 361 DNVEIMKALIVFGAEVDTNDGFTPTFLASKIGRLVTRKAILTLRTVGAECYCPPIHG 420
 Qy 396 -----QLQDLMHISPAKPAFTLGSMRDEKTRTHDL 426
 Db 421 VPAEQGSAAPHHPFSLERAQPPISLNLELQDLMHISPAKPAFTLGSMRDEKTRTHDL 480
 Qy 427 LCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRGM 486
 Db 481 LCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRGM 540
 Qy 487 YFRMKDEVFRGSRPYESGPLEEFKKEFGHTKMTDVRKPKVMTGLTSDROPAPAEHLHFR 546
 Db 541 YFRMKDEVFRGSRPYESGPLEEFKKEFGHTKMTDVRKPKVMTGLTSDROPAPAEHLHFR 600
 Qy 547 NYDAPETVREPRFNQNVNLRPPAQSDQLVWRAARSSGAAPTYFRPNGRFLDGLLANNP 606
 Db 601 NYDAPETVREPRFNQNVNLRPPAQSDQLVWRAARSSGAAPTYFRPNGRFLDGLLANNP 660

PT Novel composition comprising purified mammalian calcium independent
PT phospholipase enzyme, useful for the screening of inhibitors of
PT phospholipase activity, is active in the absence of calcium.
PS Claim 6; Page 23-25; 41pp; English.
XX
CC The invention relates to a purified mammalian calcium independent
CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
CC characterized by activity in the absence of calcium and has a molecular
CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
CC calcium independent phospholipase enzyme is useful for identifying an
CC inhibitor of phospholipase activity which involves combining (I),
CC phospholipid and candidate inhibitor compound, and observing whether the
CC enzyme cleaves the phospholipid and releases fatty acid from it. A
CC pharmaceutical composition (PC) comprising a therapeutically effective
CC amount of the inhibitor is useful for reducing inflammation and for
CC treating inflammatory conditions including rheumatoid arthritis,
CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
CC by increased levels of prostaglandins, leukotriene or platelet activating
CC factor. A composition comprising an antibody which binds to (I) is useful
CC as research and diagnostic tool, and is also useful in the study of
CC phospholipase A2 activity and inflammatory conditions. The present
CC sequence represents a human cPLA2/B enzyme longer splice variant (clone
CC 19a)
XX
SQ Sequence 687 AA;
Query Match 99.5%; Score 3606.5; DB 5; Length 687;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 MQFFGRLVNTFGVNTLFSNPFVRKVEAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGRLVNTFGVNTLFSNPFVRKVEAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLELEADALVNFHQSOLLPPFYESSQVLHTEVQLHQLTDLIRNHPWS 120
DB 61 NPNRSQSGFRLFQLELEADALVNFHQSOLLPPFYESSQVLHTEVQLHQLTDLIRNHPWS 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDDGILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDDGILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNVNNOGLTPLHLACQLGQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNVNNOGLTPLHLACQLGQEMVRVLL 240
QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNVNNOGLTPLHLACQLGQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNVNNOGLTPLHLACQLGQEMVRVLL 240
QY 241 LCNARCNIMGPNPGYPHSAKFQSKGCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNPGYPHSAKFQSKGCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKGCNVNSTSSAGNTALHVGVRNRPDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKGCNVNSTSSAGNTALHVGVRNRPDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMLKALIVGAEDVTNDPGETPTFLASKIGROLQDLMHISRKARKPAFILGSRWDEK 420
DB 361 DNVEMLKALIVGAEDVTNDPGETPTFLASKIGK-LQDLMHISRKARKPAFILGSRWDEK 419
QY 421 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWAGTSTGGILAILHLSKSM 480
DB 420 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWAGTSTGGILAILHLSKSM 479
QY 481 AYMRGMYFRMKDEVPFRGSRPYESGPIEEFLKREFGHEHTKMTDVRKPKVMTLGTLSRQPA 540
DB 480 AYMRGMYFRMKDEVPFRGSRPYESGPIEEFLKREFGHEHTKMTDVRKPKVMTLGTLSRQPA 539
QY 541 ELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLVRAARSSGAAPTFRPNRGFLDGG 600
DB 540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLVRAARSSGAAPTFRPNRGFLDGG 599
QY 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
DB 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659

DB 600 LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
QY 661 WELAKTVFGAKELGKMWVDCCTDPDGRP 688
DB 660 WELAKTVFGAKELGKMWVDCCTDPDGRP 687
RESULT 6
AAE25968
ID AAE25968 standard; protein; 806 AA.
XX AAE25968;
AC AAE25968;
XX 15-NOV-2002 (first entry)
DT Human PLA2 group VI (Ca2+-independent) protein.
XX Human; antisense; phospholipase A2; infection; inflammation; tumour;
KW antisense therapy; PLA2 protein.
XX Homo sapiens.
OS Homo sapiens.
XX US6410325-B1.
PN 25-JUN-2002.
XX 09-MAY-2001; 2001US-00851896.
PF 09-MAY-2001; 2001US-00851896.
PR (ISIS-) ISIS PHARM INC.
XX Bennett CF, Freier SM, Watt AT;
PI WPI; 2002-616513/66.
DR N-PSDB; AAD42941.
XX Novel antisense compounds useful for inhibiting gene expression of human
PT phospholipase A2, group VI and for treating diseases associated with
PT expression of phospholipase A2, group VI.
XX Disclosure; Col 109-116; 72pp; English.
XX The present invention relates to novel antisense compounds which inhibit
CC the expression of phospholipase A2 (PLA2), group VI (Ca2+-independent).
CC The invention is useful for inhibiting the expression of PLA2, group VI
CC (Ca2+-independent) in human cells or tissues and for treating an animal,
CC particularly a human suspected of having or being prone to a disease or
CC condition associated with expression of human PLA2, group VI (Ca2+-
CC independent). It is useful for diagnostics, therapeutics and as research
CC reagent, e.g. prophylactically to prevent or delay infection, tumour
CC formation or inflammation. The present sequence is human PLA2 group VI
CC (Ca2+-independent) protein
XX Sequence 806 AA;
Query Match 98.5%; Score 3572; DB 5; Length 806;
Best Local Similarity 92.4%; Pred. No. 0;
Matches 685; Conservative 1; Mismatches 1; Indels 54; Gaps 1;
QY 1 MQFFGRLVNTFGVNTLFSNPFVRKVEAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGRLVNTFGVNTLFSNPFVRKVEAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLELEADALVNFHQSOLLPPFYESSQVLHTEVQLHQLTDLIRNHPWS 120
DB 61 NPNRSQSGFRLFQLELEADALVNFHQSOLLPPFYESSQVLHTEVQLHQLTDLIRNHPWS 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDDGILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDDGILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNVNNOGLTPLHLACQLGQEMVRVLL 240

QY 661 WELAKTVFGAKELGKRWVDDCCTDPDGR 687
 DB 693 WELAKTVFGAKELGKRWVDDCCTDPDGR 719

RESULT 4

AAW17847
 ID AAW17847 standard; protein; 687 AA.

AC AAW17847;
 XX

DT 07-AUG-1997 (first entry)
 XX

DE Cytosolic phospholipase A2/B (alternatively spliced clone 19a).
 XX

KW Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
 inflammation; inhibitor; antiinflammatory.
 XX

OS Homo sapiens.
 XX

PN WO9717448-A2.
 XX

PD 15-MAY-1997.
 XX

PF 07-NOV-1996; 96WO-US017794.
 XX

PR 08-NOV-1995; 95US-00555568.
 XX

XX (GEMY) GENETICS INST INC.
 XX

PI Jones S, Tang J;
 XX

DR WPI; 1997-281037/25.
 DR N-PSDB; AAT68825.
 XX

PT Calcium independent phospholipase A2/B - used to reduce inflammation in a
 mammalian subject.
 XX

PS Claim 12; Page 49-51; 74pp; English.
 XX

CC A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17847) is
 characterised by activity in the absence of calcium, by activity in a
 mixed micelle assay with 1-palmitoyl-2-(14C)- arachidonyl-
 phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a
 lack of stimulation by ATP, and by including in its sequence at least one
 of the amino acid sequences given in AAW17839- 44). It is an
 CC alternatively spliced variant of another isolated polypeptide (AAW17845)
 and is encoded by an isolated cDNA (AAT68825). Other PLA2/B enzymes
 (AAW17846, AAW17848) have also been identified. sPLA2/B enzymes are
 thought to be involved in the release of arachidonic acid in specific
 CC tissues. Recombinant sPLA2/B polypeptides produced in transformed host
 CC cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory
 CC drugs which inhibit the arachidonic acid cascade
 XX

SQ Sequence 687 AA;

Query Match 99.5%; Score 3606.5; DB 2; Length 687;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MQFFGRLVNTFSGVTNLFNPNFRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60

DB 1 MQFFGRLVNTFSGVTNLFNPNFRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60

QY 61 NPNRSQSGRLQLELEADALVNFHOYSSQLIPFYESSPOVLHTEVLOHLTDLIRNHPWS 120

DB 61 NPNRSQSGRLQLELEADALVNFHOYSSQLIPFYESSPOVLHTEVLOHLTDLIRNHPWS 120

QY 121 SVAHLAVALGIRECFHHSRIISCANCAENEGCTPLHLACRKGDDGELVELVQYCHTQMD 180

DB 121 SVAHLAVALGIRECFHHSRIISCANCAENEGCTPLHLACRKGDDGELVELVQYCHTQMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVLLQGLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

DB 181 VTDYKGETVFHYAVQGDNSQVLLQGLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

QY 181 VTDYKGETVFHYAVQGDNSQVLLQGLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

DB 181 VTDYKGETVFHYAVQGDNSQVLLQGLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

QY 181 VTDYKGETVFHYAVQGDNSQVLLQGLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

DB 181 VTDYKGETVFHYAVQGDNSQVLLQGLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

DB 181 VTDYKGETVFHYAVQGDNSQVLLQGLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
 QY 241 LCNARCNIMGNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAQNAWA 300
 DB 241 LCNARCNIMGNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAQNAWA 300
 QY 301 RMLLRKGCNVNSTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
 DB 301 RMLLRKGCNVNSTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
 QY 361 DNVEMIKALIVFGAEVDPNDPGETPTFLASKIGROLQDLMIHSRARKPAFTLGSMRDEK 420
 DB 361 DNVEMIKALIVFGAEVDPNDPGETPTFLASKIGROLQDLMIHSRARKPAFTLGSMRDEK 420
 QY 421 RTHDHLCLDGGVKGGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480
 DB 420 RTHDHLCLDGGVKGGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 479
 QY 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEFLKREFGHEHTMTDVRKPKVMTGTLSDRQPA 540
 DB 480 AYMRGMYFRMKDEVPFRGSRPYESGPLEFLKREFGHEHTMTDVRKPKVMTGTLSDRQPA 539
 QY 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRNGRFLDGG 600
 DB 540 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRNGRFLDGG 599
 QY 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSPNP 660
 DB 600 LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSPNP 659
 QY 661 WELAKTVFGAKELGKRWVDDCCTDPDGR 687
 DB 660 WELAKTVFGAKELGKRWVDDCCTDPDGR 687

RESULT 5

ABB82231
 ID ABB82231 standard; protein; 687 AA.

AC ABB82231;
 XX

DT 08-JAN-2003 (first entry)
 XX

DE Human cPLA2/B splice variant (clone 19a).
 XX

KW Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
 antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;
 antiaschmatic; human.
 XX

OS Homo sapiens.
 XX

PN US2002106364-A1.
 XX

PD 08-AUG-2002.
 XX

PF 09-AUG-2001; 2001US-00927180.
 XX

PR 27-JUL-1994; 94US-00281193.
 PR 14-APR-1995; 95US-00422106.
 PR 14-APR-1995; 95US-00422420.
 PR 26-JUN-1995; 95WO-US008069.
 PR 08-NOV-1995; 95US-00555568.
 PR 09-SEP-1998; 98US-00149988.
 PR 06-MAR-2000; 2000US-00519223.
 XX

PA (GEMY) GENETICS INST INC.
 XX

PI Jones S, Tang J;
 XX

DR WPI; 2002-739923/80.
 DR N-PSDB; ABV73010.
 XX

Db	301	RMLLRKGCNNVNSTSSAGNTALHVGVMNRNPFDCAIIVLLTHGANADARGEHGTPLHLAMSK	360
QY	361	DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGRQLQDLMLHISRARKPAFILGSMRDEK	420
Db	361	DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGRQLQDLMLHISRARKPAFILGSMRDEK	420
QY	421	RTHDHLLCLDGGVGKGLIIQLLIAIEKASGVATKOLFQWVAGTSTGGILAILHSKSM	480
Db	421	RTHDHLLCLDGGVGKGLIIQLLIAIEKASGVATKOLFQWVAGTSTGGILAILHSKSM	480
QY	481	AYMRGMYFMKDEVRFGSRPYSGPLEEFLKRFEGEHTKMDVRKPKVMTGTLSORQA	540
Db	481	AYMRGMYFMKDEVRFGSRPYSGPLEEFLKRFEGEHTKMDVRKPKVMTGTLSORQA	540
QY	541	ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSPQLVRAARSSGAAPTFRPNGRFLDGG	600
Db	541	ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSPQLVRAARSSGAAPTFRPNGRFLDGG	600
QY	601	LLANPTLDAMTEIHEYNDLIRKGOANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP	660
Db	601	LLANPTLDAMTEIHEYNDLIRKGOANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP	660
QY	661	WELAKTVFGAKELGKMWDCCTDPDGRP	688
Db	661	WELAKTVFGAKELGKMWDCCTDPDGRP	688
RESULT 3			
ADD93407			
ID	ADD93407 standard; protein; 784 AA.		
XX			
AC	ADD93407;		
XX			
DT	29-JAN-2004 (first entry)		
XX			
DE	Human lipid-associated molecule LIPAM-14 polypeptide.		
XX			
KW	Human; lipid-associated molecule; LIPAM-14; neuroprotective; relaxant;		
KW	antihypoid; antidiabetic; cytostatic; dermatological; immunosuppressive;		
KW	antiinflammatory; thymomimetic; antiallergic; cerebroprotective;		
KW	gastrointestinal; hepatotropic; nephrotropic; anticonvulsant;		
KW	antiparkinsonian; antibacterial; antiparasitic; fungicide; protozoacide;		
KW	virucide; uteropathic; antirheumatic; cardiant; cardiovascular; anti-HIV;		
XX			
OS	Homo sapiens.		
XX			
PN	WO2003083081-A2.		
XX			
PD	09-OCT-2003.		
XX			
PF	27-MAR-2003; 2003WO-US0009755.		
XX			
PR	29-MAR-2002; 2002US-0368722P.		
XX			
PR	03-MAY-2002; 2002US-0377576P.		
XX			
PR	05-JUL-2002; 2002US-0393934P.		
XX			
PR	27-SEP-2002; 2002US-0414269P.		
XX			
PA	(INCY-) INCYTE CORP.		
XX			
PI	Emerling BM, Marquis JP, Chawla NK, Lee SY, Duggan BM, Warren BA;		
PI	Baughn MR, Lee EA, Griffin JA, Kahle AE, Elliott VS, Chang H;		
PI	Lee S, Ramkumar J, Bulloch SA, Hafalia AJA, Khare R, Jiang X;		
PI	Jackson AA;		
XX			
DR	WPI; 2003-788347/74.		
XX			
DR	N-PSDB; ADD93426.		
XX			
PT	New LIPAM polypeptides, useful for diagnosing, preventing, and treating		
PT	disorders associated with abnormal expression or activity of LIPAM, e.g.		
PT	neuromuscular, immunological, cardiovascular disorders, cancer and/or		
PT	infections.		
XX			

PS	Claim 69; Page 206-207; 238pp; English.		
XX	The present sequence is the protein sequence of human lipid-associated molecule LIPAM-14 (Incyte polypeptide 7512662CD1), a protein that shows homology to human Ca ²⁺ -independent phospholipase A2 short isoform. This is one of 19 LIPAM polypeptides of the invention. The invention relates to these novel LIPAMs and the nucleic acids encoding them, and to the use of nucleic acids and proteins in the diagnosis, treatment and prevention of disorders associated with abnormal expression or activity of LIPAM such as neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's disease), muscular disorders (e.g. myotonic dystrophy, catatonial), endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g. leukaemia, cervical or breast cancers), immunological disorders (e.g. scleroderma, systemic lupus erythematosus, allergies), gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's syndrome), infections (e.g. viral, bacterial, fungal, parasitic, protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis), or hepatic diseases (e.g. cirrhosis). The invention also relates to the assessment of the effects of exogenous compounds on the expression of nucleic acids and LIPAMs. The invention provides expression vectors, host cells, antibodies, agonists and antagonists, transgenic organisms, and arrays and microarrays of the polynucleotides.		
XX			
SQ	Sequence 784 AA;		
	Query Match	99.6%;	Score 3612; DB 7; Length 784;
	Best Local Similarity	99.9%;	Pred. No. 0;
	Matches 686;	Conservative 0;	Mismatches 1; Indels 0; Gaps 0;
QY	1	MQFFGLVNTFGSVTNLFNPNFRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV	60
Db	33	MQFFGLVNTFGSVTNLFNPNFRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV	92
QY	61	NPRNSQSGRLFOLELEADALVNFRHOYSQQLPFPYESSQVLTHTVQLHLTDLIRNHPW	120
Db	93	NPRNSQSGRLFOLELEADALVNFRHOYSQQLPFPYESSQVLTHTVQLHLTDLIRNHPW	152
QY	121	SVAHLAVALGIRECFHHSRIISCANCAENEGCTPLHLACRKGDGEILVELVOYCHTQMD	180
Db	153	SVAHLAVALGIRECFHHSRIISCANCAENEGCTPLHLACRKGDGEILVELVOYCHTQMD	212
QY	181	VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL	240
Db	213	VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL	272
QY	241	LCNARCINMGPNGYPITHSAMKFSQKCAEMIISMDSQIHSKDPRIYGASPLHWAKNAEMA	300
Db	273	LCNARCINMGPNGYPITHSAMKFSQKCAEMIISMDSQIHSKDPRIYGASPLHWAKNAEMA	332
QY	301	RMLLRKGCNNVSTSSAGNTALHVGVMNRNPDCAIIVLLTHGANADARGEHGTPLHLAMSK	360
Db	333	RMLLRKGCNNVSTSSAGNTALHVGVMNRNPDCAIIVLLTHGANADARGEHGTPLHLAMSK	392
QY	361	DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIGRQLQDLMLHISRARKPAFILGSMRDEK	420
Db	393	DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIGRQLQDLMLHISRARKPAFILGSMRDEK	452
QY	421	RTHDHLLCLDGGVGKGLIIQLLIAIEKASGVATKOLFQWVAGTSTGGILAILHSKSM	480
Db	453	RTHDHLLCLDGGVGKGLIIQLLIAIEKASGVATKOLFQWVAGTSTGGILAILHSKSM	512
QY	481	AYMRGMYFMKDEVRFGSRPYSGPLEEFLKRFEGEHTKMDVRKPKVMTGTLSDRQPA	540
Db	513	AYMRGMYFMKDEVRFGSRPYSGPLEEFLKRFEGEHTKMDVRKPKVMTGTLSDRQPA	572
QY	541	ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSPQLVRAARSSGAAPTFRPNGRFLDGG	600
Db	573	ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSPQLVRAARSSGAAPTFRPNGRFLDGG	632
QY	601	LLANPTLDAMTEIHEYNDLIRKGOANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP	660
Db	633	LLANPTLDAMTEIHEYNDLIRKGOANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP	692

```

XX SQ Sequence 688 AA;
Query Match
Best Local Similarity 100.0%; Score 3625; DB 2; Length 688;
Matches 688; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFFGRLVNTFSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGRLVNTFSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLELEADALVNFHOYSQQLPFYESSQVLHTEVLOHLDLIRNHPSW 120
DB 61 NPNRSQSGFRLFQLELEADALVNFHOYSQQLPFYESSQVLHTEVLOHLDLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEIILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEIILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQDINSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGQKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQDINSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGQKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAENA 300
DB 241 LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAENA 300
QY 301 RMLLRGCGNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRGCGNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNPDEGTPFTFLASKIGRQLOQLMHSRARKPAFTILGSMRDEK 420
DB 361 DNVEIMKALIVFGAEVDTNPDEGTPFTFLASKIGRQLOQLMHSRARKPAFTILGSMRDEK 420
QY 421 RTHDHLCLLDGGVKGGLIIQLLIIATEKASGVATKDLFDWVAGTSTGGILALAILHKSXM 480
DB 421 RTHDHLCLLDGGVKGGLIIQLLIIATEKASGVATKDLFDWVAGTSTGGILALAILHKSXM 480
QY 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEEFKEFEHTEHTQVTVRKPKNMLTGTLSDRQPA 540
DB 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEEFKEFEHTEHTQVTVRKPKNMLTGTLSDRQPA 540
QY 541 ELHLFRNYDAPETVREPFRNQNVNLRPPAQPDSQDQVWRAARSSGAAPTYFRPNRFLDGG 600
DB 541 ELHLFRNYDAPETVREPFRNQNVNLRPPAQPDSQDQVWRAARSSGAAPTYFRPNRFLDGG 600
QY 601 LIANNPTLDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPVTCYDVFRRPSNP 660
DB 601 LIANNPTLDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPVTCYDVFRRPSNP 660
QY 661 WELAKTVFGAKELGKMVVDCCDTPDGRP 688
DB 661 WELAKTVFGAKELGKMVVDCCDTPDGRP 688

RESULT 2
ID ABB82232
AC ABB82232
DE ABB82232
DT 08-JAN-2003 (first entry)
XX Human cPLA2/B splice variant (clone 19b).
DE Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
KW antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;
XX antiasthmatic; human.
OS Homo sapiens.
XX US2002106364-A1.
PN

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XX 08-AUG-2002.
XX 09-AUG-2001; 2001US-00927180.
XX 27-JUL-1994; 94US-00281193.
XX 14-APR-1995; 95US-00422106.
XX 14-APR-1995; 95US-00422420.
XX 26-JUN-1995; 95WO-US008069.
XX 08-NOV-1995; 95US-00555568.
XX 09-SEP-1998; 98US-00149988.
XX 06-MAR-2000; 2000US-00519223.
XX (GEMY ) GENETICS INST INC.
XX Jones S, Tang J;
XX WPI: 2002-739923/80.
XX N-PSDB; ABV73011.
XX Novel composition comprising purified mammalian calcium independent
PT phospholipase enzyme, useful for the screening of inhibitors of
PT phospholipase activity, is active in the absence of calcium.
XX Claim 6; Page 28-30; 41pp; English.
XX The invention relates to a purified mammalian calcium independent
CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
CC characterized by activity in the absence of calcium and has a molecular
CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
CC calcium independent phospholipase enzyme is useful for identifying an
CC inhibitor of phospholipase activity which involves combining (I),
CC phospholipid and candidate inhibitor compound, and observing whether the
CC enzyme cleaves the phospholipid and releases fatty acid from it. A
CC pharmaceutical composition (PC) comprising a therapeutically effective
CC amount of the inhibitor is useful for reducing inflammation and for
CC treating inflammatory conditions including rheumatoid arthritis,
CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
CC by increased levels of prostaglandins, leukotriene or platelet activating
CC factor. A composition comprising an antibody which binds to (I) is useful
CC as research and diagnostic tool, and is also useful in the study of
CC phospholipase A2 activity and inflammatory conditions. The present
CC sequence represents a human cPLA2/B enzyme longer splice variant (clone
CC 19b)
XX
SQ Sequence 688 AA;
Query Match 100.0%; Score 3625; DB 5; Length 688;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 688; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFFGRLVNTFSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGRLVNTFSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLELEADALVNFHOYSQQLPFYESSQVLHTEVLOHLDLIRNHPSW 120
DB 61 NPNRSQSGFRLFQLELEADALVNFHOYSQQLPFYESSQVLHTEVLOHLDLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEIILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEIILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQDINSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGQKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQDINSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGQKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAENA 300
DB 241 LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAENA 300
QY 301 RMLLRGCGNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRGCGNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:05:39 ; Search time 88.7957 Seconds
(without alignments)
2996.666 Million cell updates/sec

Title: US-10-612-668-23

Perfect score: 3625

Sequence: 1 MQFFRLVNTFGVTNLFNS.....GAKELGKMVVDCCTDPDGRP 688

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3625	100.0	688	2	AAW17848	Cytosolic
2	3625	100.0	688	5	ABB82232	Human cpl
3	3612	99.6	784	7	ADD93407	Human lip
4	3606.5	99.5	687	2	AAW17847	Cytosolic
5	3606.5	99.5	687	5	ABB82231	Human cpl
6	3572	98.5	806	5	Aae25968	Human PLA
7	3572	98.5	806	8	ADO19776	Human PRO
8	3563	98.3	810	8	ABM84355	Human dia
9	3563	98.3	810	8	ABM84354	Human dia
10	3315	91.4	752	2	AAR83018	Calcium-i
11	3315	91.4	752	2	AAW01479	Calcium-i
12	3315	91.4	752	2	AAW13163	Ca-indepe
13	3315	91.4	752	2	AAW17849	Hamster c
14	3315	91.4	752	2	AAW81825	Chinese h
15	3315	91.4	752	5	ABB82215	Calcium i
16	3269.5	90.2	751	7	AD046244	Rat Prote
17	3269.5	90.2	751	7	AD560532	Rat Prote
18	3269.5	90.2	751	7	AD552230	Rat Prote
19	3269.5	90.2	751	7	AD560536	Rat Prote
20	2728.5	75.3	667	7	ADM05093	Human pro
21	2084	57.5	394	2	AAW17845	Cytosolic
22	2084	57.5	394	5	ABB82229	Calcium i
23	1696	46.8	401	4	AAW92811	Human pro
24	1531	42.2	292	2	AAW17846	Cytosolic
25	1531	42.2	292	5	ABB82230	Calcium i

ALIGNMENTS

RESULT 1

AAW17848

ID AAW17848 standard; protein; 688 AA.

XX AC AAW17848;

DT 07-AUG-1997 (first entry)

DE Cytosolic phospholipase A2/B (alternatively spliced clone 19b) .

XX KW Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade; inflammation; inhibitor; antiinflammatory.

OS Homo sapiens.

XX WO9717448-A2.

XX PD 15-MAY-1997.

PF 07-NOV-1996; 96WO-US017794.

XX PR 08-NOV-1995; 95US-00555568.

XX (GEMY) GENETICS INST INC.

XX Jones S, Tang J;

DR WPI; 1997-281037/25.

XX N-PSDB; AAT68826.

PT Calcium independent phospholipase A2/B - used to reduce inflammation in a mammalian subject.

XX Claim 12; Page 54-56; 74pp; English.

XX A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17848) is characterised by activity in the absence of calcium, by activity in a mixed micelle assay with 1-palmitoyl-2-(14C) - arachidonyl-phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a lack of stimulation by ATP, and by including in its sequence at least one of the amino acid sequences given in AAW17839- 44). It is an alternatively spliced variant of another isolated polypeptide (AAW17846) and is encoded by an isolated cDNA (AAT68826). Other PLA2/B enzymes (AAW17845, AAW17847) have also been identified. sPLA2/B enzymes are thought to be involved in the release of arachidonic acid in specific tissues. Recombinant sPLA2/B polypeptides produced in transformed host cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory drugs which inhibit the arachidonic acid cascade


```
Db 563 LLCLDGGGIRGLVLMQLEIEKLSRTPIIHFMDWTAGTGTGGILALALGCGKTRQMG 622
Qy 486 MYFRMKDVFGRSRPYESGPLEEFKRGEGHTKMTDVRKPKVMTGLTSLDQPAELHLF 545
Db 623 LYLRKQOCFVGRSPYNSEFFESILKNDLGEFNVTDIKHPKIMVTGVNADRPVDLHLF 682
Qy 546 RNYDAPETVR---EPFNQVNLRPDPAOSDOLVWRAARSSGAAPYFRPNCGRFLDGGLL 602
Db 683 RNYTSASDILGIVTPINNRI---PPQPSQOLVWRAARATGAAPSYFRAFGRFLDGGLL 739
Qy 603 ANNPITLDMTEIHEYNQDLIRKQANKVKKLSVSLGTGRSPQVPVTCVDFVRPSNPWE 662
Db 740 ANNPITLDMTEIHEYNMALSARSAGREAI PVSVMVSLGTGHI PVTTELKDIDVFRPESIW 799
Qy 663 LAKTVFGAKELGMVDDCTDDPGR 687
Db 800 TAKLAYGISTIGNLLVDQATCS DGR 824

RESULT 12
Q8MR13 PRELIMINARY; PRT; 386 AA.
AC Q8MR13;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE LD4451Sp.
GN ORFNames=CG6718;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Friese E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY121292; AAM52704.1; -.
DR FlyBase; FBgn0036053; CG6718.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF01734; Patatin; 1.
SQ SEQUENCE 386 AA; 42693 MW; B32B7BCFC38541DD CRC64;

Query Match 20.5%; Score 741.5; DB 2; Length 386;
Best Local Similarity 43.1%; Pred. No. 4.3e-48;
Matches 155; Conservative 55; Mismatches 109; Indels 41; Gaps 4;

Qy 331 DCAIVLLTGANADARGEHTPLHLSKONVEMIKALIVCAEVDTPNDGFTFTFLA 390
Db 2 DALLGMFTTKVNAD-----EMKKNSSDLSAGSKSAVSSPEQLPSPSTPIA 49
Qy 391 SKTIGROLQDLMLHSRARKPAFILGSRNDEKRTDHLCLDGGVKGKLIILIIILIAIEKAS 450
Db 50 AEIG-----DKPYGRGLLCLDGGGIRGLVLMQLEIEKLS 86
Qy 451 GVATKDLFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDVEFRGSRPYESGPLEEPL 510
Db 87 RTPPIIHFMDWTAGTSTGGILALALGCGKTRQMGILYLRKQOCFVGRSPYNSEFFESIL 146
Qy 511 KREFGHTKMTDVRKPKVMTGLTSLDQPAELHLFRNYDAPETVR---EPFNQVNLRP 567
Db 147 KNLGFEFNVTDIKHPKIMVTGVNADRPVDLHLFRNYTSASDILGIVTPINNRI---P 203
Qy 568 PAQPSDOLVWRAARSSGAAPYFRPNCGRFLDGGLLANNPTLDMTEIHEYNQDLIRKQOA 627
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Db 204 PPQPSQOLVWRAARATGAAPSYFRAFGRFLDGGLLANNPTLDMTEIHEYNMALSARSAGRE 263
Qy 628 NKVKKLSIVSLGTGRSPQVPVTCVDFVRPSNPWEIAKTVFGAKELGMVDDCTDDPGR 687
Db 264 SEAI PVSVMVSLGTGHI PVTTELKDIDVFRPESIWDTAKLAYGISTIGNLLVDQATCS DGR 323

RESULT 13
Q20500 PRELIMINARY; PRT; 1071 AA.
AC Q20500;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-WAR-2004 (TREMELrel. 26, Last annotation update)
DE Hypothetical protein F47A4.5.
GN ORFNames=F47A4.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Mortimore B.J.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z49888; CAA90061.1; -.
DR PIR; T22327; T22327.
DR WormBase; WBGene00009801; F47A4.5.
DR WormPeP; F47A4.5; C802248.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR InterPro; IPR001638; SBP bac_3.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00023; Ank; 5.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS50088; ANK_REPEAT; 3.
DR PROSITE; PS50297; ANK_REPEAT; 1.
DR PROSITE; PS01039; SBP_BACTERIAL_3; UNKNOWN_1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
KW ANK repeat; Hypothetical protein.
SQ SEQUENCE 1071 AA; 119089 MW; 138067CA3E31C1D5 CRC64;
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Query Match 18.0%; Score 651; DB 2; Length 1071;
Best Local Similarity 27.1%; Pred. No. 1.5e-40;
Matches 195; Conservative 125; Mismatches 260; Indels 140; Gaps 20;

Qy 69 FRLFOLEAEADALVNFHOYSSQLLPFYESSQVQLHTEVL---OHLTDLIRNHPWSVAH 124
Db 315 FSLFRATDKKLDMLLHLCDKEKSLFTSLDSTMTRADILRSKIEELVQIRLKPYYMH 374
Qy 125 LAVELGIRECFHHSRI-----ISCANCAENEECTPLHLACRKGDSILVELVOY 174
Db 375 VAIAITDRDLDFSDGMIKTMNETLEPFESQLRCLCHTENCYPVHLALTMDROKIVLLEL 434
Qy 175 CHTQMDVTDYKGETVFHYAVQGDNSQVLQLGRNAVAG---LNQVNNQGLTPLHLACQLG 231
Db 435 DPTLFCETDKAGNVMHVH---NSSFCAQIIWDRCPASQHFIDERNMDGQSPLEAVSTA 491
Qy 232 KQEMVRVLLLCNARCINMGPNGYPIHSAKFSOKCAEMISM-----DSS 277
Db 492 KPLVATFL-----IGKAKFTRGDRNELFVAMTSKNAQSVVEVVLTDKP 535
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DE CG6718-PB (Cg6718-pc).
GN ORFNames=CG6718;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brattier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodagat, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirkas R., Tabor P.B., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=2426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirkas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=2426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

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RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RN Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003550; AAN11936.2; -.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0045735; F: nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; ANK; 4.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS50088; ANK_REPEAT; 3.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat.
SQ SEQUENCE 887 AA; 97778 MW; 1387084E7265BEE5 CRC64;

Query Match 32.1%; Score 1165; DB 2; Length 887;
Best Local Similarity 32.2%; Pred. No 6e-80;
Matches 259; Conservative 136; Mismatches 246; Indels 164; Gaps 13;

QY 17 LFSNPRVKEVAVADYSSDRVREGQLILFQNTPNRTWDCVLVNPNSQSGFLRFLQLEL 76
DB 17 LFSNPRVKEVAVADYSSDRVREGQLILFQNTPNRTWDCVLVNPNSQSGFLRFLQLEL 76
DB 50 LFAPPE-----NSSNEKRAVVEIILQRTSD-----SNTTSFSLRSPV 88
QY 77 EADALVNFHOYSQLLPFVSESPQVLTETVLQHLTLIRNHPNSVAHLAVALGIGRECFH 136
DB 77 EADALVNFHOYSQLLPFVSESPQVLTETVLQHLTLIRNHPNSVAHLAVALGIGRECFH 136
DB 89 QQEAERFNAFLQRLPFVSVIKEYVYNNVNGLOKACDALADNPSTLTHLHAYFNLDYIS 148
QY 137 HSRITSCANCAENEGCTPLHLACRKGDEILVELVOYCHTQMDVTDYKGTWFHVAVOG 196
DB 137 HSRITSCANCAENEGCTPLHLACRKGDEILVELVOYCHTQMDVTDYKGTWFHVAVOG 196
DB 149 NPKMLQCVDQADAAITLMSFPQLAIQGHMVKALLPL--SKLEHLDINSNSVFHAA-S 205
QY 197 DNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLLLCNARCINMGPI 256
DB 197 DNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLLLCNARCINMGPI 256
DB 206 TTKEIINLIIDKSTVNLNHLNSDGYTPLHVACLADKPNVKKALLAGANVNL---NAKDI 262
QY 257 HSAMKFSQKCAEMIISMDSSQIHSDPRYGPASPLHWAKNAEMARMLKRGCVNSTSSA 316
DB 257 HSAMKFSQKCAEMIISMDSSQIHSDPRYGPASPLHWAKNAEMARMLKRGCVNSTSSA 316
DB 263 RKVYKTSAPTTSVSSFLRTNVQMDKQYGLTGLHWCSSRETTLHALIMEGCDVNAITFD 322
QY 317 GNTALHVGVMNRFDCAIVLLTHGANADARGHGNTPLHLAMSKONVMIKALIVFGAEV 376
DB 317 GNTALHVGVMNRFDCAIVLLTHGANADARGHGNTPLHLAMSKONVMIKALIVFGAEV 376
DB 323 GTALHVVVARNRFEVCVTLHADEAIDVLDKGNALHAIIEKKLVPIVQCLVVFCDI 382
QY 377 DTFNDFGETP-----TFLASKIG----- 394
DB 377 DTFNDFGETP-----TFLASKIG----- 394
DB 383 NLKNKDGKTPRHVMGNDASGNKDDIYLHSVGAKRCKDTGSKCPCPGCNKNGNIGPP 442
QY 395 -----RQLQDLMI-----SR-----ARKPAFI----- 412
DB 395 -----RQLQDLMI-----SR-----ARKPAFI----- 412
DB 443 EAPESVEQREHTEHMLATTSRQMMGFLNAAANGILEKQQAQPKPVVVDTEKELQGQSIM 502
QY 413 -----LGSNR----- 425
DB 413 -----LGSNR----- 425
DB 503 DALLGNFTTKVNADEMKKENSDDSLASGQSKAVSSPEQLPSTPSIAAIEIGDKPYGRGR 562
QY 426 LCLDGGGVKGLIIIIQLLIAIEKASGVATKOLFVWVAGTSTGILALAILHSSKSMAYMRG 485

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Db	600	YKSTATFQPLTVQGHEDDELLLVGYTRPPRKRVKVTDEBQLVWRAARSSGAAPTVPFRM	659
Qy	594	GRFDGGLANNPTLDAMTEIHEYNODLIRKQANKVKKLSIVVSLGTGRSPQVPTCV	653
Db	660	GRFDGGLANNPTLDAMTEIHFQNKALKKQGRDEVDVRLGVVSLGTGKPPQVANSVD	719
Qy	654	VFRPSNPWELAKTVFGAKELGKVMVDCCTDPDG	686
Db	720	VFRPSNPWELAKTVFGVKGELGKMLVDCCTDSG	752
RESULT 9			
ID	Q7Q2U1	PRELIMINARY; PRT; 879 AA.	
AC	Q7Q2U1;		
DT	01-MAR-2004 (TrEMBLrel. 26, Created)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	EbiP3359 (Fragment)		
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OS	Anopheles gambiae str. PEST.		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.		
OX	NCBI_TaxID=180454;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=PEST;		
RA	Anopheles Genome Sequencing Consortium;		
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.		
CC	-!- CAUTION: The sequence shown here is derived from an		
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is		
CC	preliminary data.		
DR	EMBL; AAB01008968; EAA13225.1; -.		
DR	HSSP; P20749; 1K1B.		
DR	GO; GO:0003824; F:catalytic activity; IEA.		
DR	GO; GO:0045735; F:nutrient reservoir activity; IEA.		
DR	InterPro; IPR002110; ANK.		
DR	InterPro; IPR000560; HisAc phsptse.		
DR	InterPro; IPR002641; Patatin.		
DR	Pfam; PF00023; Ank; 6.		
DR	Pfam; PF01734; Patatin; 1.		
DR	PRINTS; PR01415; ANKYRN.		
DR	PROSITE; PS00088; ANK REPEAT; 3.		
DR	PROSITE; PS0297; ANK REP REGION; 1.		
DR	PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.		
KW	ANK repeat.		
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Best Local Similarity 32.1%; Score 1165.5; DB 2; Length 879;			
Matches 260; Conservative 132; Mismatches 272; Indels 145; Gaps 8;			
Qy	21	PFRVAVADYTSRDSRREEGQLILFQNTNPNR-----TWDCVLNPNRS--QSGRLFQ	73
Db	11	PNKQVEKNESYNLNPVLQNESMRLEFAPNPNSPDKLYVEILRPHSETINTSLSLR	70
Qy	74	LEADALNVHFQYSSQLLPFFYESSPQVLHTEVLQHLTLIRNHPSPVAHLAVELGIRE	133
Db	71	ATTQSAAEKFEAFHQRLPELVKIVREMYNINGLQKLCVDLIDNPSWSLAHVAFYNLTD	130
Qy	134	CFHHSIIISCANCAENEBGCTPLHACRGDGEILVELVQYCHTQMDVTDYKGETVFHYA	193
Db	131	YISNPSIIDFLDYAEYSSEMTPLQVAVKANNIEFVKALIQSNQCNLEHLDKNSNVFHYA	190
Qy	194	VQGDNSVQLQLGRNAVAGLVNNGQLTPLHLACQLGKQEMVRVLLLCNARCININGPNG	253
Db	191	A-STTKEMINMLTAKTSNLNHCNTGTGYPPLHLACLADPCDCKVALLLAGADTNKVA-RG	248
Qy	254	YPIHSAMKFSQKCAEMIISDSSQIHSKDPYRGASPLHWAKNAEMRLKRGCVNST	313
Db	249	AGTSYSKSIPISSNADFLVS-NDPKLFTQDMKHGGTPLHWSSREVLINSIIEGCDNLV	307

Qy	314	SSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKALIVFG	373
Db	308	NFNGQTPHLVWVARDLECVALLADAEIDVVDNSGNTPLHIAVEKKLPIVQCLVVF	367
Qy	374	AEVDPNDPGEPTPTFLASKIGRQLQDLM-----	401
Db	368	ADFNKENKDGKTPRHLVGKDDSGSKDSMLYLHLSVGAKRCPKSGKCPGCAAGGTNG	427
Qy	402	-----HISRA	406
Db	428	IPPAQPETTEOREHIQOVLARTTTKSHRNSVPISLINTIRATIPERERPEVKTVDSOE	487
Qy	407	RKPAFILGSM-----RDEKRTHD-----	424
Db	488	RKGASMDALLSMFMSKVEAASKPTSPSTSSSLKECAGSGQRTSRPRSSCEAGASGE	547
Qy	425	-----HLLCLDGGGVKGLIIQLLIAIEKASGAVATKDLFDWVAGTSTGGILALHLSK	478
Db	548	SYNGRGLLCLDGGGIRGLVLAQMLLEIENLAQTPIVHLFDWITAGTSTGGILALALCGCK	607
Qy	479	SMAYWRCMYFRMKDEVFRGSRPYESGPLFEFLKREGEHTMTDVRKPKVNLGTGTSDRQ	538
Db	608	TKQCNCCLYLRMKDQAFVGSRPYPSQLTEVLKEQLGEFTVMSDIKHPRMLVMTGVMDRK	667
Qy	539	PAELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDOLVWRAARSSGAAPTVFRPNGRFLD	598
Db	668	PVNLHLFRNYEAASDILSVTSPNNRGQPPPPSEQLVWRAARATGAAPSYFRAFGRFLD	727
Qy	599	GGLANNPTLDAMTEIHEYNODLIRKQANKVKKLSIVVSLGTGRSPQVPTCVDFVRPS	658
Db	728	GGLANNPTLDAMTEIHELNAALHYIGRASEAVPVSVVSLGTGLTPVVDLKEIDVFRPD	787
Qy	659	NPWELAKTVFGAKELGKVMVDCCTDPDGR	687
Db	788	SIWATAKVAYGISTITSLVLDQATASDGR	816
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ID	Q9VT60	PRELIMINARY; PRT; 877 AA.	
AC	Q9VT60;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	CG6718-PA.		
GN	ORFNames=CG6718;		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;		
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,		
RA	Abriel J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,		
RA	Balaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,		
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,		
RA	Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,		
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,		

QY 121 SVAHLAVELGIRECPHSHSIIISCANCAENEBEGCTPLHLACRKGDEGILLVELVVOYCHTQMD 180
Db 121 SLAHVAVEIGLSEFKHSHLSNSTCDGSGTTLPLHLACKGDNCLQELVEECQARLD 180
QY 181 VTDYKGETVFHYAVOQDINSQVLLGRNAVAGLNVNNOGLTPLHLACOLGQOEMVRVLL 240
Db 181 IADQNGEVTYHAAQONNPRVIEILCSVPSGVNHKSNNNETPLHVACRLGKTELVLALL 240
QY 241 LCNARCNMGPNGYPIHSAMKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 RCHARDIITGDKGYPIHTAMKYSQKECVBAIILDSASQLHAEDPRYQATPIHWAKNAEMA 300
QY 301 RMLKRGCCNVNSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHGNTPHLHMSK 360
Db 301 RLIIERGNCVNSTCKTDLPLHIMVKRDFEAMVLLTNVADPNVKGHEHGNTPHLHMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDGCTPTFLASKIGLOQLMHISRRK----PAFTLGSM 416
Db 361 DQLELIKALMWFGADVQEHNDGCTPTFLIAARSSKGRDFVYVSTALSGMLVPQDVTDR 420
QY 417 REKTRTHLLCLDGGGVKGLIIQLLIAEKASGVATKDLFDWVAGTSGTGILALAILH 476
Db 421 EDGLRVKDRLLCLDGGGIRGLVLMQLLIAIEKAAGRPIRELFDMVSGTSGTGILALAIH 480
QY 477 SKSMAYMGMVFRMKDEVERGSRPYESGPLEBFLKEEGEHTKMTDVRKPKVMTCTLSD 536
Db 481 GMPMSVRCLYFRMKNEVPHGRSPYESGPLEBFLKEEGEHTKMTDVRKPKVMTCTLSD 540
QY 537 ROPAEHLHFRNYDAPETVREPRFNQNVNLRPPAQSDQLVWRAARSSGAAPTYFRPNGRF 596
Db 541 RHPAEHLHFRNYDPPETDHEPPYKSVASFRVPTTAEQOLVWHAARSSGAAPTYLRPMGRF 600
QY 597 LDGGLLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIVSLGTRSPQVPTCVTDVDR 656
Db 601 LDGGLLSNPTLDAMTEIHEYNTCLKKGMAGQVKLGIWVSLGTCKPQIISVSGSVDR 660
QY 657 PSNPVELATVFCAGELGKQWVDCCTDPDG 686
Db 661 PSNPVEWMTVVGARELGKQWVDCCTDSDG 690

RESULT 8

Q6NWY0 PRELIMINARY; PRT; 818 AA.
AC Q6NWY0;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE ZGC:77476.
GN ORFNames=ZGC:77476;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina M., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC067375; AAH67375.1; --
DR HSSP; P20749; 1K1B
DR ZFIN; ZDB-GENE-040426-2079; zgc:77476.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0045735; F: nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS00297; ANK_REPEAT_REGION; 1.
KW ANK repeat.
SQ SEQUENCE 818 AA; 90691 MW; C7B5CD45401F8EA9 CRC64;
Query Match 54.5%; Score 1974; DB 2; Length 818;
Best Local Similarity 50.5%; Pred. No. 7, 7e-142;
Matches 380; Conservative 122; Mismatches 183; Indels 68; Gaps 4;

QY 1 MQPFRLVNTSGVNTLFSNPRVKEVAVADYTSDDRVREBQQLILPONTNRTWDCVLV 60
Db 1 MQPFLGRILDTVSSVSLSFNPRVDRVQLSDYNGKILHQEGRLALYRNQSQSDCLLL 60
QY 61 NPNRSQSGFRLEADALVNFHQSOLLPPFYESSPVLHTVLOHLTLIRNHPGW 120
Db 61 CPESPSVALRFPQVASEEDAMNFFQYALKRPFTFEMLRPPLPKPEMLQIVDCVRNHPW 120
QY 121 SVAHLAVELGIRECPHSHSIIISCANCAENEBEGCTPLHLACRKGDEGILLVELVVOYCHTQMD 180
Db 121 SSHAIAVDTGLRDLCKHNVILSQMN-SRDAQOCTPLHLACERGDVGVCRELEECQARTD 179
QY 181 VTDYKGETVFHYAVOQDINSQVLLGRNAVAGLNVNNOGLTPLHLACOLGQOEMVRVLL 240
Db 180 VKDKNGETPMHCAAKQDSALIIIEVLCAQICAGVSNELNAAGETPMHACRLGVEVVKGLL 239
QY 241 LCNARCNMGPNGYPIHSAMKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
Db 240 AGGARCDIINGNGFPFIHTAMKFSKSCAAILUSSPNQLLAEDPVYGGTFLHWAKTAMS 299
QY 301 RMLKRGCCNVNSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHGNTPHLHMSK 360
Db 300 RLIIERGNCVNSTCKTDLPLHIMVKRDFEAMVLLTNVADPNVKGHEHGNTPHLHMSK 359
QY 361 DNVEIMKALIVFGAEVDTNDGCTPTFLASKI----- 393
Db 360 DNMDLIKALMWFGADVQEHNDGCTPTFLIAARSSKGRDFVYVSTALSGMLVPQDVTDR 419
QY 394 -----GRQLQDLMHIS---RARKPAFILGSMRDEKTRTHDHLCLDGGGVKGLI 438
Db 420 SPTHSLRKAPPGIGDFDIMQVAVAVTAMSRGFFVADGLKTKGNKMDRLCLDGGGIGKGLV 479
QY 439 ITQLLIAIEKASGVATKDLFDWVAGTSGTGILALIAILHSKSMAYMGMVFRMKDEVRFS 498
Db 480 LIQLLIAIEKASGVATKDLFDWVAGTSGTGILALIAI VHGSWEYLRCLYFRMKDEVRFS 539
QY 499 RPYESGPLEEFLKREFGHEHTKMTDVRKPKVMTCTLSDRQPAELHLFRNYDAPETVDR 558
Db 540 RPYESGPLEEFLKREFGHEHTKMTDVRKPKVMTCTLSDRQPAELHLFRNYDAPETVDR 599
QY 559 FNQNVNLPAPAP-----SDQLVWRAARSSGAAPTYFRPN 593

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DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANK; 6.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Hypothetical protein.
SQ SEQUENCE 807 AA; 89555 MW; 1B9018AE1B2D252F CRC64;

Query Match 90.1%; Score 3267.5; DB 2; Length 807;
Best Local Similarity 83.6%; Pred. No. 9.9e-241;
Matches 620; Conservative 31; Mismatches 36; Indels 55; Gaps 1;

QY 1 MOFFGRLVNTFSGVTLNFSNPRVAVAVADYTSDDRVREEGQLILFQNTPTNRTWDCVLV 60
DB 1 MOFFGRLVNTFSGVTLNFSNPRVAVAVADYTSDDRVREEGQLILFQNTPTNRTWDCVLV 60

QY 61 NPNRSQSGRLFOLELEADALVNFHFOYSSOLLFPFYESSPOVLHTEVLQHLTDLIRNHPW 120
DB 61 SPNPSQSGRLFOLESEADALVNFQYSSQLPFYESSQVLHVEVLQHLTDLIRNHPW 120

QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDSILVELVOYCHTQMD 180
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEEGCTPLHLACRKGDSILVELVOYCHTQMD 180

QY 181 VTDYKETVFHYAVQDNGSOVLQLGRNAVAGLVNQNQGLTPLHLACQLGQEMVRVLL 240
DB 181 VTDNKGETAHYAVQDNGSOVLQLGKNASAGLVNQNQGLTPLHLACQLGQEMVRVLL 240

QY 241 LCNARCNIMPNGVPIYTHSAMKFSQKCAEMIISMDSSQTHSDPRYGPASPLHWAKNAWA 300
DB 241 LCNARCNIMPNGVPIYTHAMKFSQKCAEMIISMDSNQIHSKDPRIYGPASPLHWAKNAWA 300

QY 301 RMLLKGCVNNTSSAGNTALHVGVMNRPFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKGCDVNSTASGNTALHVAVTNRFDVCMVLLTYGANAGARGEHNTPLHLAMSK 360

QY 361 DNVEMTKALIVGAEDVTDNDFGTTFLASKIGR----- 395
DB 361 DNMVMKALIVGAEDVTDNDFGTTFAFASKISKILTRKALITLLKTVGADYHFPFIQ 420

QY 396 -----OLDLAMHISRAKPAFILGSMRDEKETHD 425
DB 421 VSTEQSSAGPHFFSLDRTPPTISLNLEQLDLPVSRARPAFILGSMRDEKETHD 480

QY 426 LLCLDGGVKGGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRG 485
DB 481 LLCLDGGVKGGLVIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRG 540

QY 486 MYPRMKDEVGRSRPYESGPLEBFLKREGEHTKMTDVKPKVMTGTTLSDRQPAELHLF 545
DB 541 VYPRMKDEVGRSRPYESGPLEBFLKREGEHTKMTDVKPKVMTGTTLSDRQPAELHLF 600

QY 546 RNYDAETVREPFNQNVLRLPPAOPSQDLVWAARSAGAAPTYFRPNGRELDGGLANN 605
DB 601 RNYDAEAVREPRCTTNINLKPPTQADQLVWAARSAGAAPTYFRPNGRELDGGLANN 660

QY 606 PTLIDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNPWELAK 665
DB 661 PTLIDAMTEIHEYNQDMIRKQGNKVKLSIVVSLGTGKSPQVPVTCVDVFRPSNPWELAK 720

QY 666 TVFGAKELGMVVDCCTDDPGR 687
DB 721 TVFGAKELGMVVDCCTDDPGR 742

RESULT 7
Q6DDKO PRELIMINARY; PRT; 756 AA.
AC Q6DDKO;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
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DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MGC83523 protein.
GN Name=MGC83523;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]_TaxID=8355;
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/gvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loughlan N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Klein S., Gerhard D.S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC077558; AAH77558.1; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 7.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 7.
DR PROSITE; PS50088; ANK_REPEAT; 3.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat.
SQ SEQUENCE 756 AA; 84303 MW; C0278741CCA52A71 CRC64;

Query Match 61.1%; Score 2216; DB 2; Length 756;
Best Local Similarity 59.7%; Pred. No. 2.2e-160;
Matches 412; Conservative 121; Mismatches 153; Indels 4; Gaps 1;

QY 1 MOFFGRLVNTFSGVTLNFSNPRVAVAVADYTSDDRVREEGQLILFQNTPTNRTWDCVLV 60
DB 1 MDLFGRIFTVTSVAVTNLFSNPKREVPLSEYSGSSCLQDGERMLYRNRTAKSLDCVLV 60

QY 61 NPNRSQSGRLFOLELEADALVNFHFOYSSOLLFPFYESSPOVLHTEVLQHLTDLIRNHPW 120
DB 61 NPNRSQSGRLFOLELEADALVNFHFOYSSOLLFPFYESSPOVLHTEVLQHLTDLIRNHPW 120
DB 61 NPNRSQSGRLFOLELEADALVNFHFOYSSOLLFPFYESSPOVLHTEVLQHLTDLIRNHPW 120
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OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Pancreatic islets;
RA MEDLINE=97269008; PubMed=9111008; DOI=10.1074/jbc.272.17.11250;
RA MA Z., Ramanadham S., Kempe K., Chi X.S., Ladenson J., Turk J.;
RT "Pancreatic islets express a Ca²⁺-independent phospholipase A2 enzyme
RT that contains a repeated structural homologous to the integral
RT membrane protein binding domain of ankyrin."
RL J. Biol. Chem. 272:11118-11127(1997).
CC -!- FUNCTION: Catalyzes the release of fatty acids from phospholipids.
CC It has been implicated in normal phospholipid remodeling, nitric
CC oxide-induced or vasopressin-induced arachidonic acid release and
CC in leukotriene and prostaglandin production. May participate in
CC fas mediated apoptosis and in regulating transmembrane ion flux in
CC glucose-stimulated B-cells.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a carboxylate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Found in brain, lung, spleen, kidney, liver,
CC heart and skeletal muscle.
CC -!- SIMILARITY: Contains 7 ANK repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U51898; AAC53136.1; -.
DR HSP; Q60778; LOY3.
DR RGD; 628867; Pla2g6.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; Ank; 6.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Hydrolase; Lipid degradation; Repeat.
FT REPEAT 150 180 ANK 1.
FT REPEAT 184 214 ANK 2.
FT REPEAT 218 247 ANK 3.
FT REPEAT 250 280 ANK 4.
FT REPEAT 285 311 ANK 5.
FT REPEAT 315 344 ANK 6.
FT REPEAT 348 377 ANK 7.
FT ACT_SITE 464 464 Potential.
SQ SEQUENCE 751 AA; 83582 MW; 393BBBADA7FCC99B CRC64;
Query Match 90.2%; Score 3269.5; DB 1; Length 751;
Best Local Similarity 89.7%; Pred. No. 6.3e-241;
Matches 616; Conservative 30; Mismatches 40; Indels 1; Gaps 1;
QY 1 MQPFGRLVTFSGVTLFSPNPRFKVAVADYTSDDRVREBQGLILFQNTPRTWDCVLV 60
DB 1 MQPFGRLVNTLSSTVTLFSPNPRFKVAVADYTSDDRVREBQGLILFQNTPRTWDCVLV 60
QY 61 NPNRSQSGPLFQLEADALVNFHGYSSQLLPFYESSQVLHTEVLQHLTDLIRNHPSW 120
DB 61 SPNRSQSGPLFQLEADALVNFHGYSSQLLPFYESSQVLHTEVLQHLTDLIRNHPSW 119
QY 121 SVAHLAVELGIRCFHHSRIISCAENAEBCGTPHLACRKGDSGLVVELVOYCHTQMD 180
DB 120 TVTHLAVELGIRCFHHSRIITCANSTENEGCTPLHLACRKGDSGLVVELVOYCHTQMD 179
QY 181 VTDYKGETVFHYAQGDSQVQLLGRNAVAGLNQVNNQGLTPLHLACQKGQEMVRVLL 240
DB 180 VTDNKGETAFAHYAQGDSQVQLLGRNAVAGLNQVNNQGLTPLHLACQKGQEMVRVLL 239
QY 241 LCNARCNIWPGNYPTSHAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEWA 300

Db 240 LCNARCNIWPGNYPTSHAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEWA 299
QY 301 RMLKRGCVNNTSAGNTALHVGVMRNFCAIVLLTHGANADARGHGNTPPLHLAMSK 360
DB 300 RMLKRGCDVSTASGNTALHVAVTRNRFDCVMVLLTYGANAGARGHGNTPPLHLAMSK 359
QY 361 DNVMEMIKALIVFGAEVDTPNDFGETPTLASKIGLOLDLMIHSPARKPAPFLLGSMRDEK 420
DB 360 DNMEVVKALIVFGAEVDTPNDFGETPTAFIASKISQLOLDLMPVSRARPAFLLGSMRDEK 419
QY 421 RTHDHLCLDGGVKGKLIILQLLIAEKASGVATKDLFDWVAGTSTGGILALILHLSKM 480
DB 420 RTHDHLCLDGGVKGKLIILQLLIAEKASGVATKDLFDWVAGTSTGGILALILHLSKM 479
QY 481 AYMRGMYFRMKDEVPFRGSRPYESGLPFLKREGEHTKMTDVRPKVMLTGLTSDRQPA 540
DB 480 AYMRGMYFRMKDEVPFRGSRPYESGLPFLKREGEHTKMTDVRPKVMLTGLTSDRQPA 539
QY 541 ELHLFRNYDAPETVREPFRNQNVLPRPAQPSDQLVWRAARSSGAAPTYFRPNGRFLDGG 600
DB 540 ELHLFRNYDAPETVREPFRNQNVLPRPAQPSDQLVWRAARSSGAAPTYFRPNGRFLDGG 599
QY 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNP 660
DB 600 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNP 659
QY 661 WELAKTVFGAKELGKQWVDCCTDDPGR 687
DB 660 WELAKTVFGAKELGKQWVDCCTDDPGR 686
RESULT 6
Q66HD1 PRELIMINARY; PRT; 807 AA.
ID Q66HD1;
AC Q66HD1;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Hypothetical protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Ljueliano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richardson D.K., Muzny K.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Small U., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Testis;
RC Director MGC Project;
RA Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC081916; AAH81916.1; -.

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QY 541 ELHLFRNYDAETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTFRPNRGFLDGG 600
Db 541 ELHLFRNYDAEAVREPRCNQNLKPTQPADQLVWRAARSSGAAPTFRPNRGFLDGG 600
QY 601 LIANNPTLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
Db 601 LIANNPTLDAMTEIHEYNQDMIRKQGNKVKLSIVVSLGTGKSPQVPVTCVDVFRPSNP 660
QY 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687
Db 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 4
Q9JK61
ID Q9JK61 PRELIMINARY; PRT; 807 AA.
AC Q9JK61
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ca2+-independent phospholipase A2 long form (Pla2g6 protein).
GN Name-Pla2g6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIH/Swiss;
RA Chiu C.-H., Jackowski S.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,
RA Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smaluk D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF259401; AAF72651.1; -.
DR EMBL; BC057209; AAH57209.1; -.
DR HSSP; Q60778; 1OY3.
DR MGD; MGI:1859152; Pla2g6.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
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KW ANK repeat.
SQ SEQUENCE 807 AA; 89559 MW; 3838889731100294 CRC64;

Query Match          90.2%; Score 3271.5; DB 2; Length 807;
Best Local Similarity 83.7%; Pred. No. 4.9e-241;
Matches 621; Conservative 31; Mismatches 35; Indels 55; Gaps 1;

QY 1 MOFFGRLVNTFSGVNLFSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MOFFGRLVNTLSSVTNLFNSNPRVKEVSLTDYVSSERVREEGQLILLQNVSNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLELEADALVNFIHQYSSQLLPFYESSQVLTHTVLOHLTDLIRNHPSW 120
Db 1 SPNPNQSGFRLFQLESEADALVNFQFSQLPFPFYESSQVLTHTVLOHLTDLIRNHPSW 120
QY 121 SYAHLAVELGIRECFHSHRIISCANCAENEBCGTPHLACRKGDDGILVELVVOYCHTMD 180
Db 121 TVTHLAVELGIRECFHSHRIISCANSTENEBCTPLHLACRKGDSILVELVVOYCHTMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLLRNNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDNGETAFHYAVQGDNPQVLQLLGNASAGLNVNNOGLTPLHLACCKMGKQEMVRVLL 240
QY 241 LCNARCNIIMPNGYPIHSAMKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNIIMPNGFPPIHTAMKFSQKCAEMIIISMDSNQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRKGCNVNSTSAGNTALHVGWVRNPFCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLRKGCVDVSTSSGNTALHVAVMNRNFDVVMVLLTYGANAGARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDFTGPTFLASKIGR----- 395
Db 361 DNMEVKALIVFGAEVDTNDFTGPTFLASKIGR----- 395
QY 396 -----QLQDLMHISIRARKKPAFILSSMRDEKRTDHH 425
Db 421 VSTEQSSAAATHPLFSLDRTPAISPALNNLEQLQDLMPISARKKPAFILSSMRDEKSHDH 480
QY 426 LILCLDGGVKGILLIQLLIAIEKASGVATKIDPDMVAGTSTGGILALAILHKSMAVMRG 485
Db 481 LILCLDGGVKGILLIQLLIAIEKASGVATKIDPDMVAGTSTGGILALAILHKSMAVMRG 540
QY 486 MYFRMKDVFGRSRRPVSFSGPLEFLKREGEHTKMTDVRKPKVMTGTLSDRQPAELHLF 545
Db 541 VYFRMKDVFGRSRRPVSFSGPLEFLKREGEHTKMTDVRKPKVMTGTLSDRQPAELHLF 600
QY 546 RNYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTFRPNRGFLDGLLANN 605
Db 601 RNYDAPEAVREPRCNQNLKPTQPADQLVWRAARSSGAAPTFRPNRGFLDGLLANN 660
QY 606 PTLDMATEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNPWELAK 665
Db 661 PTLDMATEIHEYNQDMIRKQGNKVKLSIVVSLGTGKSPQVPVTCVDVFRPSNPWELAK 720
QY 666 TVFGAKELGKMWVDCCTDPDGR 687
Db 721 TVFGAKELGKMWVDCCTDPDGR 742

RESULT 5
PA26 RAT
ID PA26 RAT STANDARD; PRT; 751 AA.
AC P97570;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (Cal-
DE PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=Pla2g6;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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QY 1 MOFFGRLVNTSGVNTLFSNPRFVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MOFFGRLVNTSSVNTLFSNPRFVKEVSLTDYVSSRVEREGQLILQNVNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLEADALVNFHQSOLLPPFYESSQVLHTEVLOHLTLIRNHPSW 120
DB 61 SPNPNQSGFRLFQLEADALVNFQFSSQLPPFYESSQVLHTEVLOHLTLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEILVELVOYCHTQMD 180
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEECTPLHLACRKGDEILVELVOYCHAQMD 180
QY 181 VTDYKGETVHYAVQGDNSQVLLGRNAVAGLNVNNOGLTPLHLACOLGQEMVRVLL 240
DB 181 VTDNKGETAHYAVQGDNPQVLLGRKNASAGLNVNNOGLTPLHLACMKGQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAKFQSGKCAEMIISMDSQIHSKDPYRGASPLHWAENA 300
DB 241 LCNARCNIMGPGFPPIHTAMKFSQKCAEMIISMDSNQIHSKDPYRGASPLHWAENA 300
QY 301 RMLLKRGCVNSTSSAGNTALHVGVMNRFDCAIYLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRGCDVDSTSSGNTALHVAVMNRFDCAIYLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVMKALIVFGAEVDTFNDGETPTFLASKIGROLQDLMIHSRARKPAFILGSMRDEK 420
DB 361 DNMEMVKALIVFGAEVDTFNDGETPTPALIASKISQLOLQDLMPISRARKPAFILSSMRDEK 420
QY 421 RTHDHLCLLDGGVKGGLIILQLLIAEKASGVATKDLFDWVAGTSGGLALAILHKSVM 480
DB 421 RSHDHLCLLDGGVKGGLIILQLLIAEKASGVATKDLFDWVAGTSGGLALAILHKSVM 480
QY 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFKREFGEHTQMTDVRPKVMLTGTLSDRQPA 540
DB 481 AYMRGVYFRMKDEVFRGSRPYESGPLEEFKREFGEHTQMTDVKPKVMLTGTLSDRQPA 540
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RESULT 3
Q7TPX2

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ID Q7TPX2 PRELIMINARY; PRT; 752 AA.
AC Q7TPX2;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DE 01-WAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Phospholipase A2, group VI.
GN Name=Pla2g6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Eutelestomii;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He; TISSUE=Osteoblast;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong I.,
RA Stapleton M., Soares M.B., Donaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madao A., Young A.C., Shevchenko Y., Rouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Griewood J., Krizinski M.I., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Skalska U., Smalius D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He; TISSUE=Osteoblast;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052845; AAH52845.1; -.
DR HSSP; P07207; I078.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0045735; F: nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF01734; Patatin; 1.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS0297; ANK_REPEAT; 1.
KW ANK repeat.
SQ SEQUENCE 752 AA; 83717 MW; DAC3347B0E14AAFC CRC64;
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Query Match 91.1%; Score 3302; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 2.1e-243;
Matches 621; Conservative 30; Mismatches 36; Indels 0; Gaps 0;

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QY 1 MOFFGRLVNTSGVNTLFSNPRFVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MOFFGRLVNTSSVNTLFSNPRFVKEVSLTDYVSSRVEREGQLILQNVNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLEADALVNFHQSOLLPPFYESSQVLHTEVLOHLTLIRNHPSW 120
DB 61 SPNPNQSGFRLFQLEADALVNFQFSSQLPPFYESSQVLHTEVLOHLTLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEILVELVOYCHTQMD 180
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEECTPLHLACRKGDEILVELVOYCHAQMD 180
QY 181 VTDYKGETVHYAVQGDNSQVLLGRNAVAGLNVNNOGLTPLHLACOLGQEMVRVLL 240
DB 181 VTDNKGETAHYAVQGDNPQVLLGRKNASAGLNVNNOGLTPLHLACMKGQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAKFQSGKCAEMIISMDSQIHSKDPYRGASPLHWAENA 300
DB 241 LCNARCNIMGPGFPPIHTAMKFSQKCAEMIISMDSNQIHSKDPYRGASPLHWAENA 300
QY 301 RMLLKRGCVNSTSSAGNTALHVGVMNRFDCAIYLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRGCDVDSTSSGNTALHVAVMNRFDCAIYLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVMKALIVFGAEVDTFNDGETPTFLASKIGROLQDLMIHSRARKPAFILGSMRDEK 420
DB 361 DNMEMVKALIVFGAEVDTFNDGETPTPALIASKISQLOLQDLMPISRARKPAFILSSMRDEK 420
QY 421 RTHDHLCLLDGGVKGGLIILQLLIAEKASGVATKDLFDWVAGTSGGLALAILHKSVM 480
DB 421 RSHDHLCLLDGGVKGGLIILQLLIAEKASGVATKDLFDWVAGTSGGLALAILHKSVM 480
QY 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFKREFGEHTQMTDVRPKVMLTGTLSDRQPA 540
DB 481 AYMRGVYFRMKDEVFRGSRPYESGPLEEFKREFGEHTQMTDVKPKVMLTGTLSDRQPA 540
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SEQUENCE FROM N.A.
MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
Clump M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
Bagnuley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,
Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
Hunt S.B., Jones M.C., Kershaw J., Kimberley A.M., King A.,
Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd O.T.,
Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann M.T.,
McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
Odeh C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,
Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
Vaadin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyma S.,
Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
Fullon R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
Wilson R.E., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
Peyrard M., Kedra D., Serousi E., Fransson I., Tapia I., Bruder C.E.,
O'Brien K.P., Wilkinson P., Bodenreich A., Hartman K., Hu X.,
Khan A.S., Lane L., Tilahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
[7]
SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeng B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Catalyzes the release of fatty acids from phospholipids.
CC It has been implicated in normal phospholipid remodeling, nitric
CC oxide-induced or vasopressin-induced arachidonic acid release and

in leukotriene and prostaglandin production. May participate in
fas mediated apoptosis and in regulating transmembrane ion flux in
glucose-stimulated B-cells.
-!- FUNCTION: Isoform ankryrin-IPLA2-1 and isoform ankryrin-IPLA2-2,
which lack the catalytic domain, are probably involved in the
negative regulation of iPLA2 activity.
-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
acylglycerophosphocholine + a carboxylate.
-!- SUBUNIT: Forms large oligomeric 270-350 kDa structures.
-!- SUBCELLULAR LOCATION: Isoform LH-IPLA2 was found to be membrane
bound. Isoform SH-IPLA2 is cytoplasmic.
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=4;
Name=LH-IPLA2;
IsoId=O60733-1; Sequence=VSP_000278;
Name=SH-IPLA2;
IsoId=O60733-2; Sequence=VSP_000278;
Name=Ankryrin-IPLA2-1;
IsoId=O60733-3; Sequence=VSP_000281, VSP_000282;
Name=Ankryrin-IPLA2-2;
IsoId=O60733-4; Sequence=VSP_000277, VSP_000279, VSP_000280;
-!- TISSUE SPECIFICITY: Four different transcripts were found to be
expressed in a distinct tissue distribution.
-!- SIMILARITY: Contains 7 ANK repeats.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)
or send an email to license@isb-sib.ch.

EMBL; AF064594; AAC97486.1; -
EMBL; AF102988; AAD41722.1; -
EMBL; AF102988; AAD41723.1; -
EMBL; AF117692; AAD30424.1; -
EMBL; AF117677; AAD30424.1; JOINED.
EMBL; AF117678; AAD30424.1; JOINED.
EMBL; AF117679; AAD30424.1; JOINED.
EMBL; AF117680; AAD30424.1; JOINED.
EMBL; AF117681; AAD30424.1; JOINED.
EMBL; AF117682; AAD30424.1; JOINED.
EMBL; AF117683; AAD30424.1; JOINED.
EMBL; AF117684; AAD30424.1; JOINED.
EMBL; AF117685; AAD30424.1; JOINED.
EMBL; AF117686; AAD30424.1; JOINED.
EMBL; AF117687; AAD30424.1; JOINED.
EMBL; AF117688; AAD30424.1; JOINED.
EMBL; AF117689; AAD30424.1; JOINED.
EMBL; AF117690; AAD30424.1; JOINED.
EMBL; AF117691; AAD30424.1; JOINED.
EMBL; AF116267; AAF34728.1; -
EMBL; AF116252; AAF34728.1; JOINED.
EMBL; AF116253; AAF34728.1; JOINED.
EMBL; AF116254; AAF34728.1; JOINED.
EMBL; AF116255; AAF34728.1; JOINED.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:06:44 ; Search time 111.829 Seconds
(without alignments)
3150.433 Million cell updates/sec

Title: US-10-612-668-23

Perfect score: 3625

Sequence: 1 MQFFGLVNTFGVTNLFN.....GAKELGMVVDCTDPDGRP 688

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3572	98.5	806	1 PA26 HUMAN	O60733 homo sapien
2	3312	91.4	752	1 PA26 MOUSE	P97819 mus musculus
3	3302	91.1	752	2 Q7TPE2	O7tpx2 mus musculus
4	3271.5	90.2	807	2 Q9UK61	O9jk61 mus musculus
5	3269.5	90.2	751	1 PA26 RAT	P97570 rattus norv
6	3267.5	90.1	807	2 Q66HD1	Q66hd1 rattus norv
7	2216	61.1	756	2 Q6DDK0	Q6ddk0 xenopus lae
8	1974	54.5	818	2 Q6NWO0	Q6nwy0 brachydanio
9	1165.5	32.2	879	2 Q7Q2U1	O7q2u1 anopheles g
10	1165	32.1	877	2 Q9VT60	O9vt60 drosophila
11	1165	32.1	887	2 Q7KUD4	O7kud4 drosophila
12	741.5	20.5	386	2 Q8MR13	Q8mr13 drosophila
13	651	18.0	1071	2 Q20500	Q20500 caenorhabdi
14	627	17.3	1023	2 Q62398	Q62398 caenorhabdi
15	622	17.2	1021	2 Q810Q6	Q810q6 caenorhabdi
16	453.5	12.5	762	2 Q95YD2	Q95yd2 caenorhabdi
17	350	9.7	501	2 Q9NSL3	Q9ns13 caenorhabdi
18	338	9.3	843	2 P97582	P97582 rattus norv
19	338	9.3	1219	2 Q8C8R3	Q8c8r3 mus musculus
20	332	9.2	1863	2 Q723L5	Q7z3l5 homo sapien
21	332	9.2	3924	1 ANK2 HUMAN	Q01484 homo sapien
22	334	8.9	1004	2 Q7JUNZ0	Q7jnz0 caenorhabdi
23	334	8.9	1786	2 Q17344	Q17344 caenorhabdi
24	334	8.9	1809	2 Q17487	Q17487 caenorhabdi
25	334	8.9	1815	2 Q17488	Q17488 caenorhabdi
26	334	8.9	1841	2 Q8MQG0	Q8mqg0 caenorhabdi
27	334	8.9	1867	2 Q17486	Q17486 caenorhabdi
28	334	8.9	2039	2 Q17489	Q17489 caenorhabdi
29	334	8.9	6994	2 Q17343	Q17343 caenorhabdi
30	334	8.9	6994	2 Q17490	Q17490 caenorhabdi
31	319.5	8.8	1549	2 Q24241	Q24241 drosophila

RESULT 1

PA26 HUMAN

ID PA26 HUMAN STANDARD; PRT: 806 AA.
AC O60733; O75645; Q8N452; Q9UC29; Q9UIT0; Q9Y671;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (Cal-PLA2) (Group VI phospholipase A2) (GVI PLA2).
DE PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=PLA2G6; Synonyms=iPLA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2; ANKYRIN-IPLA2-1 AND ANKYRIN-IPLA2-2).
RC TISSUE=B-cell, and Testis;
RX MEDLINE=98079046; PubMed=9417066; DOI=10.1074/jbc.273.1.207;
RA Larsson P.K.A., Claesson H.-E., Kennedy B.P.;
RT "Multiple splice variants of the human calcium-independent phospholipase A2 and their effect on enzyme activity."
RL J. Biol. Chem. 273:207-214 (1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2).
RC TISSUE=Pancratic islets;
RX MEDLINE=99194813; PubMed=10092647; DOI=10.1074/jbc.274.14.9607;
RA Ma Z., Wang X., Nowatke W., Ramanadham S., Turk J.;
RT "Human pancreatic islets express mRNA species encoding two distinct catalytically active isoforms of group VI phospholipase A2 (iPLA2) that arise from an exon-skipping mechanism of alternative splicing of the transcript from the iPLA2 gene on chromosome 22q13.1."
RL J. Biol. Chem. 274:9607-9616 (1999).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=99269033; PubMed=10336645;
RA Larsson Forsell P.K.A., Kennedy B.P., Claesson H.-E.;
RT "The human calcium-independent phospholipase A2 gene. Multiple enzymes with distinct properties from a single gene."
RL Eur. J. Biochem. 262:575-585 (1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM LH-IPLA).
RC TISSUE=Testis;
RA Ansoorge W., Winkler U., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS ILE-58; GLY-63; GLN-70; ASN-183 AND THR-343.
RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Sherwood A.M., Leibauser B.J., Nickerson D.A.;
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

ALIGNMENTS

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A;Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane
A;Reference number: PC2220; MUID:95071348; PMID:7526850
A;Accession: PC2220
A;Molecule type: protein
A;Residues: 910-929 <HER>
R;Davis, L.H.; Bennett, V.
J. Biol. Chem. 265, 10589-10596, 1990
A;Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger
A;Reference number: A35443; MUID:90285190; PMID:2141335
A;Accession: A35443
A;Molecule type: protein
A;Residues: 'X', '5', 'X', '7', '12', '403-417', 'X', '419-422', 'H', '424', 'LQ', '797-800', 'L', '802-814', '862-863',
C;Genetics:
A;Gene: GDB:ANK1; ANK
A;Cross-references: GDB:118737; OMIM:182900
A;Map position: 8p11.2-8p11.2
C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing; phosphoprotein
F;2-1881/Product: ankyrin 1, erythrocyte form 1 #status predicted <MAT1>
F;2-1512,1675-1881/Product: ankyrin 2.2, erythrocyte #status predicted <MAT2>
F;2-827/Domain: 89K #status predicted <DOM1>
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F;77-109/Domain: ankyrin repeat homology <AN02>
F;110-142/Domain: ankyrin repeat homology <AN03>
F;143-171/Domain: ankyrin repeat homology <AN04>
F;172-204/Domain: ankyrin repeat homology <AN05>
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F;238-270/Domain: ankyrin repeat homology <AN07>
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F;700-732/Domain: ankyrin repeat homology <AN21>
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F;766-798/Domain: ankyrin repeat homology <AN23>
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F;828-1382/Region: spectrin binding
F;1383-1881/Domain: 55K #status predicted <DOM3>

QY 332 CAIVLITHGANNADARGEHGNTPHLHAMSNDVEMIKALIVFGAEVDTPNDFGTPTFLAS 391
Db 617 VARSLIQYGGSANABSVQGVTPHLHAAQEGHAEMVALLLSKQANGNLGNKSLTPLHLVA 676
QY 392 KIG 394
Db 677 QEG 679
Search completed: May 26, 2005, 14:20:39
Job time : 22.6953 secs

QY	499	RPYESGPLEFLKREGEHTYMTDVRKPKVNLFGTISDRQPAELHLFRNYDADETVEPR	558
Db	703	-----PVAQILYNNGAIEINSKTNAGYTPPLHVACHFGQLNMVFLVENGADVGKTRA--	754
QY	559	FNQNVNLRPPAQPSDQLVWAARSSGAAPYFRPNGRFLDGLLANNPTILDAMTEIHEYN	618
Db	755	--SYTPLHQAQAQGHNNCVRYLLENGASP-----NEQTATGQTPL-----	792
QY	619	QDLIRKQANKVKKLSIVSLGTGRSPQV--PVTCDV-PRPSNPWELAKTVFCAKE	672
Db	793	-----SIAQRLGVSVVEILRTVTTVITEITVDERYKQPONPEAMNETMSESE	843

RESULT 7
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 C:Species: Drosophila melanogaster
 C:Date: 20-Sep-1999 #sequence revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T13940
 R:Dubreuil, R.R.; Yu, J.
 A:Title: Ankyrin and beta-spectrin accumulate independently of alpha-spectrin in *Drosophila*
 A:Reference number: Z17820; MUID: 95024098; PMID: 7937942
 A:Accession: T13940
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1549 <DUB>
 A:Cross-references: UNIPROT: Q24241; EMBL: L35601; NID: g557083; PID: g557084; PIDN: AAC37208
 C:Genetics:
 A:Cross-references: FlyBase: FBgn0011747

QY	45	ILFQNTPNRTWDCVLNPNRSQSGFRLFOLEADALVNFHOYSSQL-----PFYESSP	99
Db	319	LQONAP-----ILTKTKGLSALHM-----AAQGEHDEAAHLLDNKAPDEVTV	364
QY	100	QVL-----HTEVLOHLLTLRHNPS-----WSVAHLA-----VELGIRECFH	136
Db	365	DYLTALHVAACHGVKVKALLDYKANPNARALNGFTPLHIACKKRIKNVELLIK--H	421
QY	137	HSRIISCANCAENEGCTPLHLACRGDGBILVELVQYCHTQMDVDYKGTEVFHVAQG	196
Db	422	GANI-----GATTESGLTPLHVASFMCINIVIVLLQH-EASADLPTIRGETPLHLAARA	475
QY	197	DSQVQLQLGRNAV-----	210
Db	476	NQADIIRILRSAKVDAIVREGOTPLHVASRLGNINIMLLQHGAEINQAQSNKYSAH	535
QY	211	-----AGLNQVNNQGLTPLHLACQLGQEMVRVRLLLCNARCINMGPN	252
Db	536	IAAKEGQENIVQVLENGAENNAVTKGFTPLHLACKYQKQNVVQILLONGASIDFGKN	595
QY	253	GY-PIHSAMKFSQKCAEMIISDSS-----QI--HAKD-	283
Db	596	DVTPHLVATHYNNPSIVVELLLKQGSNPLCARNGQCAIHTACKKNYLEIAMOLLOHGADV	655
QY	284	---PRYGASPLHWAK---NAEMARMILLKRCGNVNSTSSAGNTALHVGWMNRFDCAIVLL	337
Db	656	NIISKSGFSLHLAAQGNVDVMVQLLEYGV-ISAANKGLTPLHVAAQGHVIVSQILL	714
QY	338	THGANADARGEHGNTPHLHAMSNDVNEIKALIVFGAEVDTPNDFGETPTFLASKIGRQL	397
Db	715	EHGANISERTNGYTPPLHMAHYGHLDLVKFFIENDADIEWSSNIGYTPPLHQAQAQGH--	772
QY	398	QDLMHISRRKPAFILGSMDEKRTDHLILCLDGGGVKGLIIIIQLLIAIEKASGVATKDL	457
Db	773	-----IMINLLLRHKANPNALTKD-	792
QY	458	FDWVAGTSTGGIILALAILHSHKSMAY---MRGMVPRMKDVEFRGSRPYESGPLBEFLKREF	514

Query Match 8.8%; Score 319.5; DB 2; Length 1549;
 Best Local Similarity 22.3%; Pred. No. 2.7e-16;
 Matches 139; Conservative 80; Mismatches 180; Indels 223; Gaps 22;

Db 793 -----GNTALH1--ASNUGYVTVMESEKIVTSTSVINS-----IGATEEKLK--- 833
 Qy 515 GEHTKMTDVRKPKVMLTGTLSLSD 536
 Db 834 -----VMTPELMQETLLSD 847

 RESULT 8
 T42714
 C:Species: Mus musculus (house mouse)
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T42714
 R;Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Vialamas, M.; Turtzo, L.
 J. Cell Biol. 130, 313-330, 1995
 A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene 1
 the repeat domain.
 A;Reference number: Z22237; MUID:95340633; PMID:7615634
 A;Accession: T42714
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-1765 c>P>
 A;Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710551; PIDN:AAB01605
 A;Experimental source: strain C57BL/6J; kidney
 C;Genetics:
 A;Gene: Ank3
 A;Map position: 10
 A;Introns: 1587/1
 C;Superfamily: ankyrin; ankyrin repeat homology
 C;Keywords: alternative splicing

 Query Match 8.2%; Score 296; DB 2; Length 1765;
 Best Local Similarity 24.7%; Pred. No. 2.3e-14;
 Matches 112; Conservative 82; Mismatches 191; Indels 68; Gaps 18;

 Qy 124 HLAVELG----IRECFHRSRIISCANCAENEEGCTPLHLACRKGDEILVELVOYCHTOM 179
 Db 421 HVAAFMGHNVISQLMHH-----GASPNNTNVRGETALHMAARSGQAEVRYLVQ--DGAQV 475

 Qy 180 DVTDYKGETVFHVAVQGDNSOVLQLLGRNAVAGLVNQNNGLTPLHLACQLGQEMVRVL 239
 Db 476 EAKAKDQTPLHISARLGKADIVQOLLQOG-ASPNAATTSGYTPLHLAAREGHEOVAFL 534

 Qy 240 LLNARCINMGPNQY-PIHSAKFSQKGCAMIISMDSQIHSKDPRYGASPLHWA---K 295
 Db 535 LDHGASLSITTKGFTPLHVAAYKGLKLEVASILLQKSASP--DAAGKSGLTPLHVAHYD 592

 Qy 296 NAEWARMLLKRGCVNSTSSAGNTALHGVGNRRFDCAIVLLTHGANADARGEHGNTPLH 355
 Db 593 NQKVALLLLQOGASPHAAKNQGYTPLHIAAKNQMDIATSLLEYGADANAVTQGIASVH 652

 Qy 356 LAMSKONVENMIKALIVFGAEYDTPNDFGETPTFLASKIGR-QLQDLM-----HISRARKP 409
 Db 653 LAAQEGHVDVMVLLSRNANVLSNKSGLTPLHLAAQEDRVNVAEVLVNVQGAHVDAQTKM 712

 Qy 410 AFILGSMRDEKPTHDLCLDCGGVKGLIIQLLIAIEKASGVATKDLFDWAGTSTGGI 469
 Db 713 GY-----TPLHVGC-HYGNIK---IVNFLQHSKAVNAKTKN-----GY 747

 Qy 470 LALAILHKSMAVMRGMVFRMKDVFGRSRYE---SGPLEEFLKREFGEHTKMTDVRK- 525
 Db 748 TAL-----HQAQQGHTHIINVLLQNNASPNELTVNGNTALAIARRLG-YISVVDTLKV 800

 Qy 526 --PKVMLTGTLSDRQPAELHLFRNYDAPETVRE 556
 Db 801 VTSEIMTTTITEK-----HKQNVPEITWNE 825

 RESULT 9
 T42715
 C:Species: Mus musculus (house mouse)


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Db 425 PIIAMKRGKLDVSLRKMLEKQDGLTETPTGNTVHICAIKKKLIILMEKFRDQTD 484
QY 310 VNSTSGAGNTALLHGVNRRNFDCAIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKAL 369
Db 485 PERNALQOTPLTFYIKDLGLWILTSAYGVMDAQDINGNTPHLCAVTRGNTIARML 544
QY 370 IVFGAEVDTNDFGETPTFIASKI----- 393
Db 545 LCLGAKPDINKRYKESPRHIAARLTKKEAKWIDIVRALIICGAGACDDGFGICAFGCWHT 604
QY 394 -----GRLOQLD---MHIS---RARKP-AFILG-----SMRDEKRT 422
Db 605 GLTSCKTQLGSSSDSEQSMEDVRKDIHVSNDAAAPYEFVLDPTQLVERAYARNETRA 664
QY 423 HDH-----LCLDGGGVKGLIIILQLIAIEKASGVATKDL 457
Db 665 FPHEALKRVNKLKELVEKKTSNVINVLGLOGGGIRGLVTVQMLICLEAFIDRLIDY 724
QY 458 FDVVAAGTSTGGIILALILHSKSMAYMRGMYFRMKDEVFRG-SRPYBSGPLEEFLKREFGE 516
Db 725 FDMIGATSTGYIMSTWMTGSLRKAQRYVLMFKDLQDFDSWTRPYDTKTLETFIQARFGA 784
QY 517 HTKMTDVVRKPKVMTGLTSLDRQPAELHLFRNYDAPETVREPRENQNVNLRPPAQSDQLV 576
Db 785 DRLMGDIKYPRFFCTTVRADTFPVQLELLNRYLRPISEKE---NNDLGF---TDPNELTI 838
QY 577 WRAARSGRAPTYFRPN-GRFLOGGLANNPTLDAMTEIHEYNQDLIRKQANKVKLSI 635
Db 839 WKATRSSAAPTTFSASEGFIIDGGMISNNPVLIDMSDIGFYNTTCQKMRIPKVMVDMGC 898
QY 636 VVSLGTRSPQVPVTCVDVFRPNPVELAKTVFGAKELGRMVVDCCTDPDGRP 688
Db 899 VLSVGTGITPCVD-PSVFEMNDLFGMLR---GMKNLSLVVIDQATATEGAP 947

RESULT 4
S37431
N;Alternate names: ankyrin 2, neuronal long splice form - human
N;Contains: ankyrin 2, short form
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence, revision 06-Jan-1995 #text change 09-Jul-2004
C;Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569
R;Chan, W.
submitted to the EMBL Data Library, September 1993
A;Reference number: S37431
A;Accession: S37431
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-3924 <CHA>
A;Cross-references: UNIPROT:Q01484; EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g4062
R;Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.
J. Cell Biol. 114, 241-253, 1991
A;Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal a
A;Reference number: A39643; MUID:91302466; PMID:1830053
A;Accession: A39643
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2077 <OTL>
A;Cross-references: GB:X56957
A;Accession: B39643
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1443,3585-3924 <OTT>
A;Cross-references: EMBL:X56958
R;Tse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Ward,
Genomics 10, 858-866, 1991
A;Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.
A;Reference number: A40334; MUID:9209921; PMID:1833308
A;Accession: A40334
A;Molecule type: DNA
A;Residues: 463-474,'PE',477-495 <TSE>
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A;Cross-references: GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:g178648
R;Chan, W.; Kordeli, E.; Bennett, V.
J. Cell Biol. 123, 1463-1473, 1993
A;Title: 440-kD ankyrinB: structure of the major developmentally regulated domain and se
A;Reference number: A49462; MUID:94075409; PMID:8253844
A;Accession: A49462
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-3924 <REG>
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C;Genetics:

A;Gene: GDB:ANK2
A;Cross-references: GDB:127607; OMIM:106410
A;Map position: 4q25-4q27
C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing
F;2-3924/Product: ankyrin 2, long form #status predicted <MAT>
F;2-1443,3585-3924/Product: ankyrin 2, short form #status predicted <MA2>
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Best Local Similarity 27.3%; Pred. No. 1.2e-16;
Matches 100; Conservative 62; Mismatches 127; Indels 77; Gaps 9;

QY	103	HTEVLOHLD-----LIRNHPSSVAHLAVELGIRCFHH-----SRIL	141
Db	311	HDQVVELLERGAPLLARTKNGLSPLHMAAQGDHVECVKHLLOHKA	370
QY	142	SCANC-----AENEEGCTPLHLACRKGDEILVELVOY-----	174
Db	371	VAHGHYRVTKLLDKRANPNARALNGFTPLHIACKNRKIKWELLVYK	430
QY	175	-----CH-----TOMDVTYKGETVFHYAVQGDNSQVLLGRNAVAG	212
Db	431	GLTPIHVAAPMGHLNIVLLQLQNGASPDVTNIRGETALHMAARAGQ	489
QY	213	LNQVNNQGLTPLHLACQLQKQEMVRVLLLCNARCNITMGPNGY-P	271
Db	490	VDARAREQTPLHIASRLGKTEIVQLLQHMAHPDAATNGYTPHLHI	549
QY	272	ISMDSSQIHSKOPRYCASPLHWAK---NAEMARMLKRCGNVNST	328
Db	550	--LEAGAAHSLATKKGFTPLHVAAKYGSIDVAKLLQRAAADSAG	607
QY	329	RFDCAIVLTHGANADARGEHNTPLHLAMSKDNVEMIKALIVFGAE	388
Db	608	NQKVALLLLEKSGASPHATAKNGYTPHLHIAAKNQMQIASTLNYG	667
QY	389	LASKIG 394	
Db	668	LASQEG 673	

Db 466 VPAEQSAAPHPFSLERAQPPISLNLEQLDLMHISARKPAFATILGSMRDEKTRTHDL 525
QY 427 LCLDGGVKGGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSMAYMRGM 486
Db 526 LCLDGGVKGGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSMAYMRGM 585
QY 487 YFRMKDEVGRSPYESSGPLEFLKEPGEHTKMTDVRKPKVMTGTLSDRQPAELHLFR 546
Db 586 YFRMKDEVGRSPYESSGPLEFLKEPGEHTKMTDVRKPKVMTGTLSDRQPAELHLFR 645
QY 547 NYDAPETVREPFRNQVNLPRPAQPSDQLVWRAARSSGAAPTFRNGRFLDGLLANNP 606
Db 646 NYDAPETVREPFRNQVNLPRPAQPSDQLVWRAARSSGAAPTFRNGRFLDGLLANNP 705
QY 607 TLDAMTEIHEYNOQLIRKQANKVKLSIVVSLGTRSPQVPVTCVDVFRPNPNWELAKT 666
Db 706 TLDAMTEIHEYNOQLIRKQANKVKLSIVVSLGTRSPQVPVTCVDVFRPNPNWELAKT 765
QY 667 VFGAKELGRWVDDCCTDPDGR 687
Db 766 VFGAKELGRWVDDCCTDPDGR 786

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T22327
hypotheical protein F47A4.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22327
R:Mortimore, B.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z19549
A:Accession: T22327
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1071 <WIL>
A:Cross-references: UNIPROT:O20500; EMBL:Z49888; PIDN:CAA90061.1; GSPDB:GN00028; CESP:F47A4
A:Experimental source: clone F47A4
C:Genetics:
A:Gene: CESP:F47A4.5
A:Map position: X
A:Introns: 27/1; 59/2; 134/1; 199/2; 402/2; 460/3; 591/3; 634/3; 665/2; 1018/3

Query Match 18.0%; Score 651; DB 2; Length 1071;
Best Local Similarity 27.1%; Pred. No. 1.1e-42;
Matches 195; Conservative 125; Mismatches 260; Indels 140; Gaps 20;

QY 69 FRLFOLEADALVNFHQYSSQLLPYESSQVLTHTVL-----QHLTDLIRNHPNSVAH 124
Db 315 FSLFRATDKKDLMLLHLCDEKSFLLTSLDMSTMRADILRSKIEELVIOIRLKPHYHMT 374
QY 125 LAVELGIRECFHHSRI-----ISCANCAENBEGCTPLHLACRKGDGELVELVOY 174
Db 375 VAIAOTDLDFSDGMLKTNETLEPPESQLRCLCHTENCYPVHALTMDROKIVERLLEL 434
QY 175 CHTQMDVDTYKGETVPHYAVQGDNSQVQLLGRNAVAG---LNQVNNQGLTPLHLACQIG 231
Db 435 DPTLFCETCAGNVVHHV---NSSPCAQI IWDRCPASQHFIDERNMQCSPLNEAVSTA 491
QY 232 KQBMVRVLLCNARCINMGPNGYPHSAMKFSQKCAEMIISM-----DSS 277
Db 492 KPLVATFL-----IGKGAKFTRGDRNELFVAMTSKNAQSVVEVLTDRK 535
QY 278 QIHSKDPYRCASPLHWAKNAEMARMLLKR-----GCNVNSTSSAGNTALHVGVMRNFDC 333
Db 536 EIANERDALGNSAIHVALYKESINALLNRKVELGLDIDVKNAGETALLFTTRKPDLL 595
QY 334 IVLLT---HGANADARGEHNTPLHLAMS-----KDNVEMIKALIVFGAEVDTNDFGT 385
Db 596 PLLVTLVYHAGANNATDPGNTALHKSAAVDAKKISLECVKFLISAGSNPNKINLRGES 655
QY 386 PTFLASKIGROLQDLMHISRA---RKPAFILG-----SMRDE-----419

Db 656 PRHLAASL--QNQEMLAAILKAAATRCPKGYKGCRCNCRHDCSSABDEYEETLQKIRIGN 713
QY 420 -----KRTDHLCLDGGVKGGLIIQLLIAIEKASGV 452
Db 714 ESDYEKTEFTASEKLNIOQTLDSSRRGKKAKVNLISMDGGGIRGLVIOQLTAIEERLGD 773
QY 453 ATKDLFDWVAGTSTGGILALAILHLSKSMAYMRGMFRMKDEVFRG--SRPYESSGPLEFLK 511
Db 774 DIFKTFDMSAGTSTGSLMAGLATKSLREMQOQTLYLLKDRVFDGIMPYDVTQLEKFIQ 833
QY 512 REFGEHTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPFRNQVNLPRPAQ 571
Db 834 DQFGTGT--WPEIPYPRLMISAVNSEKLPVRLMARNYKPAKV-----APETP 880
QY 572 SDQLVWRAARSSGAAPTFRPN--GRFLDGLLANNPTLDAMTEIHEYNOQLIRKQANKV 630
Db 881 KEMPLWALRRSTAAPVLFKPSDEDRVIDGGIISNNPALDLMSEVHAYNRELQSGRKSDA 940
QY 631 KKLISIVSLGTRSPQVPVTCVDVFR--PSNPWELAKTVFGAKELGRWVDDCCTDPDGR 688
Db 941 VQMNVLVSFGTG---QIPSTVIETLSIDSNSPLQSIKTI---KNLAAMFIDQATASEGAP 994

RESULT 3
T26261
hypotheical protein W07A8.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26261; T26892
R:Baeham, V.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20184
A:Accession: T26261
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1023 <WIL>
A:Cross-references: UNIPROT:O62398; EMBL:Z82075; PIDN:CAB04932.1; GSPDB:GN00023; CESP:W07A8.2
A:Experimental source: clone W07A8
R:Ainscough, R.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z20281
A:Accession: T26892
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1023 <W12>
A:Cross-references: EMBL:AL021489; PIDN:CAA16371.1; GSPDB:GN00023; CESP:W07A8.2
A:Experimental source: clone Y44A6C
C:Genetics:
A:Gene: CESP:W07A8.2
A:Map position: 5
A:Introns: 32/1; 83/2; 155/3; 202/2; 240/3; 264/3; 331/2; 411/1; 479/3; 534/3; 571/2; 708/3

Query Match 17.3%; Score 627; DB 2; Length 1023;
Best Local Similarity 23.9%; Pred. No. 8.2e-41;
Matches 185; Conservative 153; Mismatches 285; Indels 150; Gaps 23;

QY 37 RVREBQGLILFQNTNRTWDCVLVNPNSQSGFRILFQLELEAD--ALVNFHQYSSQLLPF 94
Db 204 RAKEBEEL--KNKPLYLHLAITLYNENNEKYVMSLFRSHKLADVVALCERCENPELPRV 260
QY 95 YESSQV---LHTEVLQHLTDLIRNHPNSVAHVALVELGIRECFHH---SRIISCANCAE 148
Db 261 FPKNNYNIKDYLT-----IFHELNDNTWTKSVHISKIGLLEYFENMKHEKLLKYLNLIV 315
QY 149 NEEGCTPLHLACRKGDELVELVOYCHTQMDVDTYKGETVPHYAVQGDNSQVQLQL--G 206
Db 316 QPEGUSPLMIAVQNTQIETVSWMLDH--GADINILSSEGNQVHLVAATASSGGLIKILWET 374
QY 207 RNAVAGLNQVNNQGLTPLHLACQLGQKQBMVRVLLCNARCINMGPNG-----Y 254
Db 375 KKCETMINQTSNGYTPAYVA-----LINACLNSCQTLRGFGGIGQSSDSTOMAN 424
QY 255 PIHSAMKFSQ--KGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMARMLLKR---GCN 309

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:07:29 ; Search time 19.6953 Seconds
(without alignments)
3361.064 Million cell updates/sec

Title: US-10-612-668-23
Perfect score: 3625
Sequence: 1 MQFFGRLVNTFSQVTLNFSN.....GAKELGKMVVDCDTPDGRP 688

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3572	98.5	851	2 T12503	hypothetical prote
2	651	18.0	1071	2 T22327	hypothetical prote
3	627	17.3	1023	2 T26261	hypothetical prote
4	332	9.2	3924	2 S37431	ankyrin 2, neuroma
5	326	9.0	468	2 T33857	hypothetical prote
6	324	8.9	2039	2 T15347	ankyrin-related un
7	319.5	8.8	1549	2 T13940	ankyrin - fruit fl
8	296	8.2	1765	2 T42714	ankyrin 3, splice
9	296	8.2	1940	2 T42715	ankyrin 3, splice
10	296	8.2	1943	2 T42713	ankyrin 3, splice
11	296	8.2	1961	2 T42716	ankyrin 3, splice
12	296	8.2	4377	2 A55575	ankyrin 3, long sp
13	294	8.1	1856	2 B35049	ankyrin 1, erythro
14	294	8.1	1880	2 A35049	ankyrin 1, erythro
15	294	8.1	1881	1 SJHUK	ankyrin 1, erythro
16	287	7.9	1862	2 I49502	ankyrin - mouse
17	285	7.9	1848	2 S37771	ankyrin, erythrocy
18	282	7.8	397	2 T46445	hypothetical prote
19	273	7.5	1265	2 T02131	hypothetical prote
20	273	7.5	1411	2 S30355	alpha-latroinsecto
21	269.5	7.4	456	2 T24442	hypothetical prote
22	263.5	7.3	1423	1 I37275	death-associated p
23	249	6.9	791	2 T42691	hypothetical prote
24	248.5	6.9	1435	2 T32930	hypothetical prote
25	244	6.7	247	2 D84448	probable ankyrin l
26	239	6.6	426	2 AE2149	hypothetical prote
27	237	6.5	1401	2 S11527	alpha-latrotoxin p
28	236	6.5	368	2 T18184	ankyrin repeat pro
29	236	6.5	2437	2 S42612	transmembrane prot

ALIGNMENTS

RESULT 1

T12503

hypothetical protein DKFPz434A102.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999

C;Accession: T12503

R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, June 1999

A;Reference number: Z17527

A;Accession: T12503

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-851 <ANS>

A;Cross-references: EMBL:AL080187

A;Experimental source: adult testis; clone DKFPz434A102

C;Genetics:

A;Note: DKFPz434A102.1

Query Match 98.5%; Score 3572; DB 2; Length 851;
Best Local Similarity 92.4%; Pred. No. 5.2e-273;
Matches 685; Conservative 1; Mismatches 1; Indels 54; Gaps 1;

QY	1	MOFFGRLVNTFSQVTLNFSNPPFRKVEAVADYTS	DRVREEGQLILFQNTPNRTWDCVLV	60
DB	46	MOFFGRLVNTFSQVTLNFSNPPFRKVEAVADYTS	DRVREEGQLILFQNTPNRTWDCVLV	105
QY	61	NPRNSQSGFRLFQLELEADALVNFHQYSSQLLP	PFYESSQVLTHTVQLQHLTDLIRNHPWS	120
DB	106	NPRNSQSGFRLFQLELEADALVNFHQYSSQLLP	PFYESSQVLTHTVQLQHLTDLIRNHPWS	165
QY	121	SVNHLAVELGIRECFHHSRIISCANCAENEGCT	PLHLACRKGDGHLIVELVOYCHTQMD	180
DB	166	SVNHLAVELGIRECFHHSRIISCANCAENEGCT	PLHLACRKGDGHLIVELVOYCHTQMD	225
QY	181	VTDYKGETVFHVAQGDNSQVLQLGRNAVAGLN	VQNNQGLTPLHLACQLGKGEWVRVLL	240
DB	226	VTDYKGETVFHVAQGDNSQVLQLGRNAVAGLN	VQNNQGLTPLHLACQLGKGEWVRVLL	285
QY	241	LCNARCINMGPNGYPIHSAKFQSKGCAEMIIIS	MDSSQIHSKDPRYGASPLHWAKNAEMA	300
DB	286	LCNARCINMGPNGYPIHSAKFQSKGCAEMIIIS	MDSSQIHSKDPRYGASPLHWAKNAEMA	345
QY	301	RMLLKGCNNVNTSSAGNTALHVGVRNRPDCAI	VLLTHGANADARGEHGTPLHLAMSK	360
DB	346	RMLLKGCNNVNTSSAGNTALHVGVRNRPDCAI	VLLTHGANADARGEHGTPLHLAMSK	405
QY	361	DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGR	-----	395
DB	406	DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGR	-----	465
QY	396	-----	QLQDLMIHSRARKPAFILGSRVDEKRTDHL	426

:|||||

QY 241 LCNARCNMGNGYPIHSAKFSQKGAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNMGNGYPIHSAKFSQKGAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRCGNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGHGNTPLHLAMSK 360
DB 301 RMLLKRCGVDVSTSAAGNTALHVGVMNRFDCAIIVLLTHGANADARGHGNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDPFGETPTFLASKIG- LQDLMIHSRARKPAFILGSMRDEK 419
DB 361 DNVEIMKALIVFGAEVDTNDPFGETPTFLASKIG- LQDLMIHSRARKPAFILGSMRDEK 420
QY 420 RTHDLHLLCLDGGVGLIILQIIILIAIEKASGVATKDLFDWVAGTSTGGTILAILHLSKSM 479
DB 421 RIHDLHLLCLDGGVGLVLIQIIILIAIEKASGVATKDLFDWVAGTSTGGTILAILHLSKSM 480
QY 480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKWMLTGTLSDROPA 539
DB 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKWMLTGTLSDROPA 540
QY 540 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQDLVWRAARSSGAAPTYYFRNGRFLDGG 599
DB 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQDLVWRAARSSGAAPTYYFRNGRFLDGG 600
QY 600 LIANPTLDAMTEIHEYNODLRKGOANKVKLSIVVSLGTRSGRSPQVPTCDVFRPSNP 659
DB 601 LIANPTLDAMTEIHEYNODLRKGOANKVKLSIVVSLGTRSGRSPQVPTCDVFRPSNP 660
QY 660 WELAKTVFGAKELGKMWVDCCTDPOGR 686
DB 661 WELAKTVFGAKELGKMWVDCCTDPOGR 687

RESULT 15
US-08-555-568B-17
; Sequence 17, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-17

Query Match 57.6%; Score 2084; DB 2; Length 394;

Best Local Similarity 100.0%; Pred. No. 2.9e-217;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MOFFGRLVNTFSGVTNLFNSNFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MOFFGRLVNTFSGVTNLFNSNFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPRNSQSGFRLFQLELEADALVNFHOYSSQLLPFYESSQVLHTEVLOHLTDLIRNHPSW 120
DB 61 NPRNSQSGFRLFQLELEADALVNFHOYSSQLLPFYESSQVLHTEVLOHLTDLIRNHPSW 120
QY 121 SVAHLAVELGIRECPHHSRIISCANCAENEGCTPLHLACRKGDEIIVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECPHHSRIISCANCAENEGCTPLHLACRKGDEIIVELVOYCHTQMD 180
QY 181 VTDYKGETVVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQENVRVLL 240
DB 181 VTDYKGETVVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQENVRVLL 240
QY 241 LCNARCNMGNGYPIHSAKFSQKGAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNMGNGYPIHSAKFSQKGAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRCGNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGHGNTPLHLAMSK 360
DB 301 RMLLKRCGNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGHGNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDPFGETPTFLASKIG 394
DB 361 DNVEIMKALIVFGAEVDTNDPFGETPTFLASKIG 394

Search completed: May 26, 2005, 14:21:59
Job time : 27.3333 secs


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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-2

Query Match          91.2%; Score 3302.5; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MQFFGRLVNTSGVNTLFSNPRFVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
DB 1 MQFFGRLVNTLSSVTNLFNSNPRFVKEISVADYTSHERVREEGQLILFQVNSRNTWDCILV 60
QY 61 NPNRSQSGFRLFOLEADALVNFHOYSQQLPFYESSQVPLHTEVQLHTDLIRNHP 120
DB 61 SPRNPHSGFRLFOLESEADALVNFQOFSQQLPFYESSQVPLHTEVQLHTDLIRNHP 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEBECTPLHLACRKGDEIILVELVOYCHTQMD 180
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEBECTPLHLACRKGDEIILVELVOYCHTQMD 180
QY 181 VTDYKGETVHYAVQGDNSQVQLLGRNAVAGLNQVNOGGLTPLHLACQLGQEMVRVLL 240
DB 181 VTDNKGETAFAHYAVQGDNSQVQLLGRNASAGLNQVNOGGLTPLHLACQMGQEMVRVLL 240
QY 241 LCNARCNIMGNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNVMPGSGFPIHTAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRKGCNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRKGCVDVSTSAAGNTALHVAVMNRFDVCMVLLTYGANAGTPGEGHNTPLHLAISK 360
QY 361 DNVEMIKALIVFGAEVTDNDFGETPTFLASKIGK-LQDLMIHSRARKPAFTILGSMRDEK 419
DB 361 DNMEMIKALIVFGAEVTDNDFGETPTFLASKIGK-LQDLMIHSRARKPAFTILGSMRDEK 420
QY 420 RTHDHLCLDGGVKGKLIILQIIAIEKASGVATKDLFDWVAGTSTGGILALAILHSSKM 479
DB 421 RIHDHLLCLDGGVKGKLIILQIIAIEKASGVATKDLFDWVAGTSTGGILALAILHSSKM 480
QY 480 AYMRGMYFRMKDEVPFRGSRPYESGPLEEFKREFEGEHTKMTDVRKPKVMTLGTLSDRQPA 539
DB 481 AYMRGYFRMKDEVPFRGSRPYESGPLEEFKREFEGEHTKMTDVRKPKVMTLGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLVWRAARSSGAAPTFRPNRFLDGG 599
DB 541 ELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLVWRAARSSGAAPTFRPNRFLDGG 600
QY 600 LLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIVVSLGTRSPQVPVTCVDVFRPSNP 659
DB 601 LLANNPTLDAMTEIHEYNDMIRKGOANKVKLSIVVSLGTRSPQVPVTCVDVFRPSNP 660
QY 660 WELAKTVFGAKELGKMWVDCCTDPGR 686
DB 661 WELAKTVFGAKELGKMWVDCCTDPGR 687
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RESULT 12

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US-09-519-223-2
; Sequence 2, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-519-223-2

Query Match          91.2%; Score 3302.5; DB 3; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MQFFGRLVNTSGVNTLFSNPRFVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
DB 1 MQFFGRLVNTLSSVTNLFNSNPRFVKEISVADYTSHERVREEGQLILFQVNSRNTWDCILV 60
QY 61 NPNRSQSGFRLFOLEADALVNFHOYSQQLPFYESSQVPLHTEVQLHTDLIRNHP 120
DB 61 SPRNPHSGFRLFOLESEADALVNFQOFSQQLPFYESSQVPLHTEVQLHTDLIRNHP 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEBECTPLHLACRKGDEIILVELVOYCHTQMD 180
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEBECTPLHLACRKGDEIILVELVOYCHTQMD 180
QY 181 VTDYKGETVHYAVQGDNSQVQLLGRNAVAGLNQVNOGGLTPLHLACQLGQEMVRVLL 240
DB 181 VTDNKGETAFAHYAVQGDNSQVQLLGRNASAGLNQVNOGGLTPLHLACQMGQEMVRVLL 240
QY 241 LCNARCNIMGNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNVMPGSGFPIHTAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRKGCNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRKGCVDVSTSAAGNTALHVAVMNRFDVCMVLLTYGANAGTPGEGHNTPLHLAISK 360
QY 361 DNVEMIKALIVFGAEVTDNDFGETPTFLASKIGK-LQDLMIHSRARKPAFTILGSMRDEK 419
DB 361 DNMEMIKALIVFGAEVTDNDFGETPTFLASKIGK-LQDLMIHSRARKPAFTILGSMRDEK 420
QY 420 RTHDHLCLDGGVKGKLIILQIIAIEKASGVATKDLFDWVAGTSTGGILALAILHSSKM 479
DB 421 RIHDHLLCLDGGVKGKLIILQIIAIEKASGVATKDLFDWVAGTSTGGILALAILHSSKM 480
QY 480 AYMRGMYFRMKDEVPFRGSRPYESGPLEEFKREFEGEHTKMTDVRKPKVMTLGTLSDRQPA 539
DB 481 AYMRGYFRMKDEVPFRGSRPYESGPLEEFKREFEGEHTKMTDVRKPKVMTLGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLVWRAARSSGAAPTFRPNRFLDGG 599
DB 541 ELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLVWRAARSSGAAPTFRPNRFLDGG 600
QY 600 LLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIVVSLGTRSPQVPVTCVDVFRPSNP 659
DB 601 LLANNPTLDAMTEIHEYNDMIRKGOANKVKLSIVVSLGTRSPQVPVTCVDVFRPSNP 660
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QY 301 RMLLRKGCNNVSTSSAGNTALHVGVMNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRKGCDDVSTSSAAGNTALHVGVMNRNRPDCVMVLLTYGANAGTPEGHNTPLHLAISK 360
QY 361 DNVEIMKALIVFCAEVDVTDNDTGETPTFLASKIGK-LQDLMHISRARKPAFILGSMRDEK 419
DB 361 DNMEMIKALIVFCAEVDVTDNDTGETPTFLASKIGK-LQDLMHISRARKPAFILGSMRDEK 420
QY 420 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 479
DB 421 RIHDLHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480
QY 480 AYMRGMYFRMKDEVFGRSGRPYESGLEEFLEEFKREFEGHTKMTDVRKPKVMTGTLSDRQPA 539
DB 481 AYMRGMYFRMKDEVFGRSGRPYESGLEEFLEEFKREFEGHTKMTDVRKPKVMTGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVIREPRENQNVNLRPPAQPSPDQVWRAARSSGAAPTFRPNRGFLDGG 599
DB 541 ELHLFRNYDAPETVIREPRENQNVNLRPPAQPSPDQVWRAARSSGAAPTFRPNRGFLDGG 600
QY 600 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
DB 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
QY 660 WELAKTVFGAKELGKMWVDCCTDPDGR 686
DB 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 10
US-08-735-716-2
; Sequence 2, Application US/08735716
; Patent No. 5840511
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,716
; FILING DATE: 23-OCT-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-735-716-2

Query Match 91.2%; Score 3302.5; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MOFFGRLVNTFSQVNTLFSNPRVKEVAVADYTSDDVRVEEGQLILFQNTPRNTWDCVLY 60
DB 1 MOFFGRLVNTLSSVNTLFSNPRVKEISVADYTSHERVREEGQLILFQNASRNTWDCILV 60
QY 61 NPNRSQSGFRLFOLEADALVNFHOYSQQLLPFYESSQVLHTEVQLHLDLIRNHPGW 120
DB 61 SPNPHSGFRLFOLEADALVNFQFSQQLPPFYESSQVLHTEVQLHLDLIRNHPGW 120
QY 121 SVANLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRGDGBILVELVQYCHTQMD 180
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRGDGBILVELVQYCHQAMD 180
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QY 181 VTDYKGETVFHYAVQCDNSQVQLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDNRGETAFHYAVQCDNSQVQLQLGKNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAWKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNVMGPGSPFIHTAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRKGCNNVSTSSAGNTALHVGVMNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRKGCDDVSTSSAAGNTALHVGVMNRNRPDCVMVLLTYGANAGTPEGHNTPLHLAISK 360
QY 361 DNVEIMKALIVFCAEVDVTDNDTGETPTFLASKIGK-LQDLMHISRARKPAFILGSMRDEK 419
DB 361 DNMEMIKALIVFCAEVDVTDNDTGETPTFLASKIGK-LQDLMHISRARKPAFILGSMRDEK 420
QY 420 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 479
DB 421 RIHDLHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480
QY 480 AYMRGMYFRMKDEVFGRSGRPYESGLEEFLEEFKREFEGHTKMTDVRKPKVMTGTLSDRQPA 539
DB 481 AYMRGMYFRMKDEVFGRSGRPYESGLEEFLEEFKREFEGHTKMTDVRKPKVMTGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVIREPRENQNVNLRPPAQPSPDQVWRAARSSGAAPTFRPNRGFLDGG 599
DB 541 ELHLFRNYDAPETVIREPRENQNVNLRPPAQPSPDQVWRAARSSGAAPTFRPNRGFLDGG 600
QY 600 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
DB 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
QY 660 WELAKTVFGAKELGKMWVDCCTDPDGR 686
DB 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 11
US-08-555-568B-2
; Sequence 2, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
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QY 546 NYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRPNGRFLDGLLANNP 605
Db 614 NYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRPNGRFLDGLLANNP 673
QY 606 TLDAMTEIHEYNODLIRKQANKVKKLSVWSLGTGRSPQVPVTCVDVFRPNPNWELAKT 665
Db 674 TLDAMTEIHEYNODLIRKQANKVKKLSVWSLGTGRSPQVPVTCVDVFRPNPNWELAKT 733
QY 666 VFGAKELGKMVVDCCTDPDGR 686
Db 734 VFGAKELGKMVVDCCTDPDGR 754

RESULT 8
US-08-281-193-2
; Sequence 2, Application US/08281193
; Patent No. 5466595
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-281-193-2

Query Match 91.2%; Score 3302.5; DB 1; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MOFFGRLVNTSGVTLNFSNPRVKEVAVADYTSDDRVREEGQLILFONTPNRTWDCVLV 60
Db 1 MOFFGRLVNTSSVTLNFSNPRVKEISVADYTSHERVREEGQLILFQNASNRTWDCILV 60
QY 61 NPNRSQSGFRFLQLELEADALVNFHQYSSQLPPFYESSQVLTHTVQLHQLTLIRNHPSW 120
Db 61 SPRNPHSGFRFLQLESEADALVNFQFSSQLPPFYESSQVLTHTVQLHQLSLIRSHPSW 120
QY 121 SVAHLAVALGIRECFHSHRIISCANCAENEGCTPLHLACRKGDSGLVVELVQYCHTQMD 180
Db 121 TVTHLAVALGIRECFHSHRIISCANSTENEGCTPLHLACRKGDSGLVVELVQYCHAQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVTLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
Db 181 VTDNKGETAFAHYAVQGDNSQVTLQLLGNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
QY 241 LCNARCNINMGNGYPIHSAKFSSQKCAEMIISMDSSQIHSDKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNVNGSGFPPIHTAMKFSQKCAEMIISMDSSQIHSDKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRCGNVNSTSAGNTALHVGVMNRNFDCAIVLLTHGANADAGEHNTPLHLAMSK 360
Db 301 RMLLKRCGDVSTSAAGNTALHVMNRNFDCAIVLLTHGANAGTGEHNTPLHLAISK 360
QY 361 DNVMIKALIVFGAEVTDPTDFGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 419
Db 361 DNWEMIKALIVFGAEVTDPTDFGETPTAFWASKISKQLQDLMPISRARKPAFILLSMRDEK 420
QY 420 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMM 479
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Db 421 RIHDHLLCLDGGVGKGLVLIQLLIAIERKASGVATKDLFDWVAGTSTGGILALAILHKSMM 480
QY 480 AYMRGMVFRMKDEVPFRGSRPYESGPLEEFKREFGHEHTKMTDVRKPKVWMLTCTLSDRQPA 539
Db 481 AYMRGVYFRMKDEVFRGSRPYESGPLEEFKREFGHEHTKMTDVKKPKVWMLTCTLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRPNGRFLDGG 599
Db 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRPNGRFLDGG 600
QY 600 LLANNPTLDAMTEIHEYNODLIRKQANKVKKLSVWSLGTGRSPQVPVTCVDVFRPNPN 659
Db 601 LLANNPTLDAMTEIHEYNODLIRKQANKVKKLSVWSLGTGRSPQVPVTCVDVFRPNPN 660
QY 660 WELAKTVFGAKELGKMVVDCCTDPDGR 686
Db 661 WELAKTVFGAKELGKMVVDCCTDPDGR 687

RESULT 9
US-08-422-106-2
; Sequence 2, Application US/08422106
; Patent No. 5589170
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,106
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-422-106-2

Query Match 91.2%; Score 3302.5; DB 1; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MOFFGRLVNTSGVTLNFSNPRVKEVAVADYTSDDRVREEGQLILFONTPNRTWDCVLV 60
Db 1 MOFFGRLVNTSSVTLNFSNPRVKEISVADYTSHERVREEGQLILFQNASNRTWDCILV 60
QY 61 NPNRSQSGFRFLQLELEADALVNFHQYSSQLPPFYESSQVLTHTVQLHQLTLIRNHPSW 120
Db 61 SPRNPHSGFRFLQLESEADALVNFQFSSQLPPFYESSQVLTHTVQLHQLSLIRSHPSW 120
QY 121 SVAHLAVALGIRECFHSHRIISCANCAENEGCTPLHLACRKGDSGLVVELVQYCHTQMD 180
Db 121 TVTHLAVALGIRECFHSHRIISCANSTENEGCTPLHLACRKGDSGLVVELVQYCHAQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVTLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
Db 181 VTDNKGETAFAHYAVQGDNSQVTLQLLGNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
QY 241 LCNARCNINMGNGYPIHSAKFSSQKCAEMIISMDSSQIHSDKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNVNGSGFPPIHTAMKFSQKCAEMIISMDSSQIHSDKDPYRGASPLHWAKNAEMA 300
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-927-180-23

Query Match 99.6%; Score 3606.5; DB 4; Length 688;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MQPFGRLVNTFSGVTNLFNSNPPRVKEVAVADYTSDDRVREBQGLILFQNTPNRTWDCVLV 60
DB 1 MQPFGRLVNTFSGVTNLFNSNPPRVKEVAVADYTSDDRVREBQGLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGRLFOLELEADALVNFHOYSSQLLPFYESSQVLTHTVQLHTLDLIRNHPWS 120
DB 61 NPNRSQSGRLFOLELEADALVNFHOYSSQLLPFYESSQVLTHTVQLHTLDLIRNHPWS 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDGRIILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDGRIILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPRIYGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPRIYGASPLHWAKNAEMA 300
QY 301 RMLLKRCGNVNTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCGNVNTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDPFGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 419
DB 361 DNVEIMKALIVFGAEVDTNDPFGETPTFLASKIGRLQDLMIHSRARKPAFILGSMRDEK 420
QY 420 RTHDHLCLDGGVKGILLIIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHLSKSM 479
DB 421 RTHDHLCLDGGVKGILLIIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHLSKSM 480
QY 480 AYMRGMVFRMKDVFRRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPA 539
DB 481 AYMRGMVFRMKDVFRRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPRNQNVNLPAPQPSDQLVWRAARSGAAPTFRNGRFLDGG 599
DB 541 ELHLFRNYDAPETVREPRNQNVNLPAPQPSDQLVWRAARSGAAPTFRNGRFLDGG 600
QY 600 LIANPFLDAMTEIHYNDOLIRKQANKVKLSIVVSLGTGRSPQVPTCDVDFRPSNP 659
DB 601 LIANPFLDAMTEIHYNDOLIRKQANKVKLSIVVSLGTGRSPQVPTCDVDFRPSNP 660

QY 660 WELAKTVFGAKELGKMVVDCTDPPDGRP 687
DB 661 WELAKTVFGAKELGKMVVDCTDPPDGRP 688

RESULT 7
US-09-949-016-10948
Sequence 10948, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10948
LENGTH: 819
TYPE: PRT
ORGANISM: Human
US-09-949-016-10948

Query Match 98.5%; Score 3566.5; DB 4; Length 819;
Best Local Similarity 92.3%; Pred. No. 0;
Matches 684; Conservative 1; Mismatches 1; Indels 55; Gaps 1;

QY 1 MQPFGRLVNTFSGVTNLFNSNPPRVKEVAVADYTSDDRVREBQGLILFQNTPNRTWDCVLV 60
DB 14 MQPFGRLVNTFSGVTNLFNSNPPRVKEVAVADYTSDDRVREBQGLILFQNTPNRTWDCVLV 73
QY 61 NPNRSQSGRLFOLELEADALVNFHOYSSQLLPFYESSQVLTHTVQLHTLDLIRNHPWS 120
DB 74 NPNRSQSGRLFOLELEADALVNFHOYSSQLLPFYESSQVLTHTVQLHTLDLIRNHPWS 133
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDGRIILVELVOYCHTQMD 180
DB 134 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDGRIILVELVOYCHTQMD 193
QY 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 194 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 253
QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPRIYGASPLHWAKNAEMA 300
DB 254 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPRIYGASPLHWAKNAEMA 313
QY 301 RMLLKRCGNVNTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 314 RMLLKRCGNVNTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 373
QY 361 DNVEIMKALIVFGAEVDTNDPFGETPTFLASKIGK----- 395
DB 374 DNVEIMKALIVFGAEVDTNDPFGETPTFLASKIGRLVTRKAILTLARTVGAECYCPPIHG 433
QY 396 -----LQDLMIHSRARKPAFILGSMRDEKRTDHL 425
DB 434 VPAEQGSAAPHHPFSLERAQPPPISLNNLEQLQDLMIHSRARKPAFILGSMRDEKRTDHL 493
QY 426 LCLDGGVKGILLIIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHLSKSMAYMRGM 485
DB 494 LCLDGGVKGILLIIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHLSKSMAYMRGM 553
QY 486 YFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPAELHLFR 545
DB 554 YFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPAELHLFR 613

QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIIISMDSSQIHSKDPYKASPLHAKNAEVA 300
DB 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIIISMDSSQIHSKDPYKASPLHAKNAEVA 300
QY 301 RMLLKRCGCVNSTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCGCVNSTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDPGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 419
DB 361 DNVEIMKALIVFGAEVDTNDPGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 420
QY 420 RTHDHLCLDGGVKGKLIIOQLIAIEKASGVATKDLFDWVAGTSGGILALAILHLSKSM 479
DB 421 RTHDHLCLDGGVKGKLIIOQLIAIEKASGVATKDLFDWVAGTSGGILALAILHLSKSM 480
QY 480 AYMRGMVFMKDEVPFRSGRPYESGPLEEFLKREFGEHTKMTDVRKPKVMTGTLSDRQPA 539
DB 481 AYMRGMVFMKDEVPFRSGRPYESGPLEEFLKREFGEHTKMTDVRKPKVMTGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQLVWRAARSSGAAPTYYFRPNRFLDGG 599
DB 541 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQLVWRAARSSGAAPTYYFRPNRFLDGG 600
QY 600 LIANNPTLDAMTEIHEYNOQLIRKQANKVKLSIIVSLGTGRSPQVPVTCYDVFPRSPNP 659
DB 601 LIANNPTLDAMTEIHEYNOQLIRKQANKVKLSIIVSLGTGRSPQVPVTCYDVFPRSPNP 660
QY 660 WELAKTVFGAKELGKMVVDCCCTDPDGRP 687
DB 661 WELAKTVFGAKELGKMVVDCCCTDPDGRP 688

RESULT 5

US-09-519-223-23
; Sequence 23, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-519-223-23
Query Match 99.6%; Score 3606.5; DB 3; Length 688;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 MQFFGRLVNTSGVNTLFSNPRVKEVAVADYTSSDRVREEGQLILFQNTNRTWDCVLV 60
DB 1 MQFFGRLVNTSGVNTLFSNPRVKEVAVADYTSSDRVREEGQLILFQNTNRTWDCVLV 60
QY 61 NPNRSQSQRFLFOLELEADALVNFHOYSSQLLPFYESSPOVLHTEVLOHLTLIRNHPSW 120
DB 61 NPNRSQSQRFLFOLELEADALVNFHOYSSQLLPFYESSPOVLHTEVLOHLTLIRNHPSW 120
QY 121 SVAHLAVELGIRECFPHSRIRIISCANCAENEGCTPLHLACRKGDEIILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFPHSRIRIISCANCAENEGCTPLHLACRKGDEIILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLOLLGRNAVAGLNQVNOGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLOLLGRNAVAGLNQVNOGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIIISMDSSQIHSKDPYKASPLHAKNAEVA 300
DB 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIIISMDSSQIHSKDPYKASPLHAKNAEVA 300
QY 301 RMLLKRCGCVNSTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCGCVNSTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDPGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 419
DB 361 DNVEIMKALIVFGAEVDTNDPGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 420
QY 420 RTHDHLCLDGGVKGKLIIOQLIAIEKASGVATKDLFDWVAGTSGGILALAILHLSKSM 479
DB 421 RTHDHLCLDGGVKGKLIIOQLIAIEKASGVATKDLFDWVAGTSGGILALAILHLSKSM 480
QY 480 AYMRGMVFMKDEVPFRSGRPYESGPLEEFLKREFGEHTKMTDVRKPKVMTGTLSDRQPA 539
DB 481 AYMRGMVFMKDEVPFRSGRPYESGPLEEFLKREFGEHTKMTDVRKPKVMTGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQLVWRAARSSGAAPTYYFRPNRFLDGG 599
DB 541 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQLVWRAARSSGAAPTYYFRPNRFLDGG 600
QY 600 LIANNPTLDAMTEIHEYNOQLIRKQANKVKLSIIVSLGTGRSPQVPVTCYDVFPRSPNP 659
DB 601 LIANNPTLDAMTEIHEYNOQLIRKQANKVKLSIIVSLGTGRSPQVPVTCYDVFPRSPNP 660
QY 660 WELAKTVFGAKELGKMVVDCCCTDPDGRP 687
DB 661 WELAKTVFGAKELGKMVVDCCCTDPDGRP 688

RESULT 6

US-09-927-180-23
; Sequence 23, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match 100.0%; Score 3620; DB 4; Length 687;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFFGLVNTFSGVTNLFSPNPRFVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGLVNTFSGVTNLFSPNPRFVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60

QY 61 NPNRSQSGFRLFOLEADALVNFHOYSSQLLPFYESSQVLTHTVQLHQLTDLIRNHPWS 120
Db 61 NPNRSQSGFRLFOLEADALVNFHOYSSQLLPFYESSQVLTHTVQLHQLTDLIRNHPWS 120

QY 121 SVAHLAVALGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEILVELVQYCHTQMD 180
Db 121 SVAHLAVALGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEILVELVQYCHTQMD 180

QY 181 VTDYKGETVPHYAVQGDNSQVLLQGLGRNAVAGLQVNNQGLTPLHLACQLGKQEMVRVLL 240
Db 181 VTDYKGETVPHYAVQGDNSQVLLQGLGRNAVAGLQVNNQGLTPLHLACQLGKQEMVRVLL 240

QY 241 LCNARCNIMGPNGYPIHSAKMFQKGAEMIISMDSSQIHSDKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNIMGPNGYPIHSAKMFQKGAEMIISMDSSQIHSDKDPYRGASPLHWAKNAEMA 300

QY 301 RMLLKRCGNVNTSSAGNTALHVGVMNRPFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLKRCGNVNTSSAGNTALHVGVMNRPFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360

QY 361 DNVEMTKALIVFGAEVDTNDFGETPTFLASKTGKLDLMHISRAKRPAPILGSMDEKR 420
Db 361 DNVEMTKALIVFGAEVDTNDFGETPTFLASKTGKLDLMHISRAKRPAPILGSMDEKR 420

QY 421 THDHLCLDGGVKGKLIILQLLTAIEKASGVATKDLFDWVAGTSTGGILALALILHKSMA 480
Db 421 THDHLCLDGGVKGKLIILQLLTAIEKASGVATKDLFDWVAGTSTGGILALALILHKSMA 480

QY 481 YMRGMYFRMKDEVFRGSRPYESGPLEFLKREFGHEKMTDVRKPKVMTLGTLSDRQPAE 540
Db 481 YMRGMYFRMKDEVFRGSRPYESGPLEFLKREFGHEKMTDVRKPKVMTLGTLSDRQPAE 540

QY 541 LHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQVWRAARSSGAAPTYFRPNGRFLDGGGL 600
Db 541 LHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQVWRAARSSGAAPTYFRPNGRFLDGGGL 600

QY 601 LANNPTLDAMTEIHEYNOQLIRKGQANKYKLSIVVSLGTGRSPQVPTVCTVDVFRPSNPW 660
Db 601 LANNPTLDAMTEIHEYNOQLIRKGQANKYKLSIVVSLGTGRSPQVPTVCTVDVFRPSNPW 660

QY 661 ELAKTVFGAKELGKMVWDCCTDPDGRP 687
Db 661 ELAKTVFGAKELGKMVWDCCTDPDGRP 687

RESULT 4
US-08-555-568B-23
; Sequence 23, Application US/085555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-555-568B-23

Query Match 99.6%; Score 3606.5; DB 2; Length 688;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MQFFGLVNTFSGVTNLFSPNPRFVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGLVNTFSGVTNLFSPNPRFVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60

QY 61 NPNRSQSGFRLFOLEADALVNFHOYSSQLLPFYESSQVLTHTVQLHQLTDLIRNHPWS 120
Db 61 NPNRSQSGFRLFOLEADALVNFHOYSSQLLPFYESSQVLTHTVQLHQLTDLIRNHPWS 120

QY 121 SVAHLAVALGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEILVELVQYCHTQMD 180
Db 121 SVAHLAVALGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEILVELVQYCHTQMD 180

QY 181 VTDYKGETVPHYAVQGDNSQVLLQGLGRNAVAGLQVNNQGLTPLHLACQLGKQEMVRVLL 240
Db 181 VTDYKGETVPHYAVQGDNSQVLLQGLGRNAVAGLQVNNQGLTPLHLACQLGKQEMVRVLL 240

QY 121 SVAHLAVELGIRECPHHSRIISCANCAENEECTPLHLACRKGDEIIVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECPHHSRIISCANCAENEECTPLHLACRKGDEIIVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVOGDINSQVQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVOGDINSQVQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAMKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNGYPIHSAMKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRGCNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRGCNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGKQLQDLMIHSRARKPAFIIIGSMRDEKR 420
DB 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGKQLQDLMIHSRARKPAFIIIGSMRDEKR 420
QY 421 THDHLCLDGGGVKGLIIIIQLLIAIEKASGVATKOLFDMVAGTSTGGIILALAILHKSMA 480
DB 421 THDHLCLDGGGVKGLIIIIQLLIAIEKASGVATKOLFDMVAGTSTGGIILALAILHKSMA 480
QY 481 YMRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKVMTGTLSDRQPAE 540
DB 481 YMRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKVMTGTLSDRQPAE 540
QY 541 LHLFRNYDAPETVREPFRNQVNLPPAQPSPDLVWRAARSSGAAPTFRPNRFLDGL 600
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QY 601 LANPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPTVCDVFRPSNPW 660
DB 601 LANPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPTVCDVFRPSNPW 660
QY 661 ELAKTVFGAKELGKMWVDCCTDPDGRP 687
DB 661 ELAKTVFGAKELGKMWVDCCTDPDGRP 687

RESULT 2

US-09-519-223-21
; Sequence 21, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-519-223-21

Query Match 100.0%; Score 3620; DB 3; Length 687;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MQFFGLVNTSGVTNLFNPFVRKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVILV 60
QY 61 NPNRSQSGFRLEADALVNFHQYSSQLLPFYESSPQVLHTEVLOHLDLIRNHPSW 120
DB 61 NPNRSQSGFRLEADALVNFHQYSSQLLPFYESSPQVLHTEVLOHLDLIRNHPSW 120
QY 121 SVAHLAVELGIRECPHHSRIISCANCAENEECTPLHLACRKGDEIIVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECPHHSRIISCANCAENEECTPLHLACRKGDEIIVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVOGDINSQVQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVOGDINSQVQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAMKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNGYPIHSAMKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRGCNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRGCNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGKQLQDLMIHSRARKPAFIIIGSMRDEKR 420
DB 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGKQLQDLMIHSRARKPAFIIIGSMRDEKR 420
QY 421 THDHLCLDGGGVKGLIIIIQLLIAIEKASGVATKOLFDMVAGTSTGGIILALAILHKSMA 480
DB 421 THDHLCLDGGGVKGLIIIIQLLIAIEKASGVATKOLFDMVAGTSTGGIILALAILHKSMA 480
QY 481 YMRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKVMTGTLSDRQPAE 540
DB 481 YMRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKVMTGTLSDRQPAE 540
QY 541 LHLFRNYDAPETVREPFRNQVNLPPAQPSPDLVWRAARSSGAAPTFRPNRFLDGL 600
DB 541 LHLFRNYDAPETVREPFRNQVNLPPAQPSPDLVWRAARSSGAAPTFRPNRFLDGL 600
QY 601 LANPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPTVCDVFRPSNPW 660
DB 601 LANPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPTVCDVFRPSNPW 660
QY 661 ELAKTVFGAKELGKMWVDCCTDPDGRP 687
DB 661 ELAKTVFGAKELGKMWVDCCTDPDGRP 687

RESULT 3

US-09-927-180-21
; Sequence 21, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:08:24 ; Search time 25.3333 Seconds
(without alignments)
2024.365 Million cell updates/sec

Title: US-10-612-668-21

Perfect score: 3620

Sequence: 1 MOFFGRLVNTFSGVTNLFNS.....GAKELGKMVVDCTPDGGRP 687

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
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- 5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3620	100.0	687	2	US-08-555-568B-21
2	3620	100.0	687	3	US-09-519-223-21
3	3620	100.0	687	4	US-09-527-180-21
4	3606.5	99.6	688	2	US-08-555-568B-23
5	3606.5	99.6	688	3	US-09-519-223-23
6	3606.5	99.6	688	4	US-09-527-180-23
7	3566.5	98.5	819	4	US-09-949-016-10948
8	3302.5	91.2	752	1	US-08-281-193-2
9	3302.5	91.2	752	1	US-08-422-106-2
10	3302.5	91.2	752	2	US-08-735-716-2
11	3302.5	91.2	752	2	US-08-555-568B-2
12	3302.5	91.2	752	3	US-09-519-223-2
13	3302.5	91.2	752	4	US-09-527-180-2
14	3302.5	91.2	752	5	PCT-US95-08069-2
15	2084	57.6	394	2	US-08-555-568B-17
16	2084	57.6	394	3	US-09-519-223-17
17	2084	57.6	394	4	US-09-527-180-17
18	1531	42.3	292	2	US-08-555-568B-19
19	1531	42.3	292	3	US-09-519-223-19
20	1531	42.3	292	4	US-09-527-180-19
21	1163.5	32.1	896	4	US-09-270-767-46130
22	902.5	24.9	545	4	US-09-270-767-61684
23	371	10.2	143	4	US-09-270-767-33298
24	338	9.3	843	2	US-09-172-977-3
25	338	9.3	843	4	US-09-404-108-3
26	332	9.2	1839	2	US-09-172-977-4
27	332	9.2	1839	4	US-09-404-108-4

28	332	9.2	2753	4	US-09-949-016-7659	Sequence 7659, Ap
29	332	9.2	2753	4	US-09-949-016-7660	Sequence 7660, Ap
30	332	9.2	3924	4	US-09-538-092-1246	Sequence 1246, Ap
31	305.5	8.4	1745	2	US-09-031-485-33	Sequence 33, Appl
32	305.5	8.4	1745	2	US-08-847-429A-33	Sequence 33, Appl
33	305.5	8.4	1745	3	US-09-065-474-33	Sequence 33, Appl
34	305.5	8.4	1745	3	US-09-557-034-33	Sequence 2, Appli
35	302	8.3	786	4	US-09-509-802-2	Sequence 2, Appli
36	302	8.3	787	3	US-09-188-930-334	Sequence 334, App
37	302	8.3	787	4	US-09-312-283C-334	Sequence 2, Appli
38	236	8.2	1088	3	US-09-082-059-2	Sequence 2, Appli
39	236	8.2	3913	4	US-09-949-016-10933	Sequence 10933, A
40	296	8.2	4377	4	US-09-949-016-6978	Sequence 6978, Ap
41	294	8.1	1719	4	US-09-949-016-6966	Sequence 6966, Ap
42	294	8.1	1856	4	US-09-949-016-6964	Sequence 6964, Ap
43	294	8.1	1880	4	US-09-949-016-5876	Sequence 5876, Ap
44	294	8.1	1881	4	US-09-949-016-6965	Sequence 6965, Ap
45	294	8.1	1883	4	US-09-949-016-9010	Sequence 9010, Ap

ALIGNMENTS

RESULT 1
US-08-555-568B-21
; Sequence 21, Application US/085555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-21

Query Match	100.0%;	Score	3620;	DB	2;	Length	687;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	687;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Db	1	MOFFGRLVNTFSGVTNLFNSPRVKEVAVADYTSDDRVREEGQLILFONTPNRTWDCVLV	60				
QY	61	NPRNSQSGRLPQLELEADALVNFHQYSQQLLPFFYESSQVLHTEVQLHLDLIRNHPWS	120				
Db	61	NPRNSQSGRLPQLELEADALVNFHQYSQQLLPFFYESSQVLHTEVQLHLDLIRNHPWS	120				

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Job time : 95.6667 secs

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PT	infections.	
PS	Claim 69; Page 206-207; 238pp; English.	
XX	The present sequence is the protein sequence of human lipid-associated molecule LIPAM-14 (Incyte polypeptide 7512662CD1), a protein that shows homology to human Ca2+-independent phospholipase A2 short isoform. This is one of 19 LIPAM polypeptides of the invention. The invention relates to these novel LIPAMs and the nucleic acids encoding them, and to the use of nucleic acids and proteins in the diagnosis, treatment and prevention of disorders associated with abnormal expression or activity of LIPAM such as neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's disease), muscular disorders (e.g. myotonic dystrophy, catatonias), endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g. leukemia, cervical or breast cancers), immunological disorders (e.g. scleroderma, systemic lupus erythematosus, allergies), gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's syndrome), infections (e.g. viral, bacterial, fungal, parasitic, protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis), or hepatic diseases (e.g. cirrhosis). The invention also relates to the assessment of the effects of exogenous compounds on the expression of nucleic acids and LIPAMs. The invention provides expression vectors, host cells, antibodies, agonists and antagonists, transgenic organisms, and arrays and microarrays of the polynucleotides.	
XX	Sequence 784 AA;	
SQ	Query Match 99.3%; Score 3593.5; DB 7; Length 784; Best Local Similarity 99.6%; Pred. No. 0; Matches 684; Conservative 1; Mismatches 1; Indels 1; Gaps 1;	
QY	1 MOFFGRLVNTFSGVNTLFSNPRFVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60	Db 633 LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTRSPQVPTCVDFRPSNP 692
Db	33 MOFFGRLVNTFSGVNTLFSNPRFVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 92	QY 660 WELAKTVFGAKELGKMWVDCCTDPDGR 686
QY	61 NPNRSQSGRLPQLELEADALVNFHOYSQQLLPFYESSQVLHTEVQLHLDLIRNHPSW 120	Db 693 WELAKTVFGAKELGKMWVDCCTDPDGR 719
Db	93 NPNRSQSGRLPQLELEADALVNFHOYSQQLLPFYESSQVLHTEVQLHLDLIRNHPSW 152	RESULT 6
QY	121 SVAHLAVALGIRECFHSHRIISCANCAENEBCGTPHLACRKGDGSEILVELVQYCHTQMD 180	AAE25968
Db	153 SVAHLAVALGIRECFHSHRIISCANCAENEBCGTPHLACRKGDGSEILVELVQYCHTQMD 212	ID AAE25968 standard; protein; 806 AA.
QY	181 VTDYKGETVFHVAVQGDNSQVLLQGLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240	XX AAE25968;
Db	213 VTDYKGETVFHVAVQGDNSQVLLQGLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 272	XX 15-NOV-2002 (first entry)
QY	241 LCNARCNIMGPNGYPIHSAKFTSOKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAWA 300	DE Human PLA2 group VI (Ca2+-independent) protein.
Db	273 LCNARCNIMGPNGYPIHSAKFTSOKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAWA 332	XX Human; antisense; phospholipase A2; infection; inflammation; tumour;
QY	301 RMLLKRGCVNNTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360	KW antisense therapy; PLA2 protein.
Db	333 RMLLKRGCVNNTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 392	XX Homo sapiens.
QY	361 DNVEIMKALIVFGAEVDTNDPFGTFTFLASKIGK-LQDLMIHSRARKPAFILGSRDEK 419	OS US6410325-B1.
Db	393 DNVEIMKALIVFGAEVDTNDPFGTFTFLASKIGK-LQDLMIHSRARKPAFILGSRDEK 452	PN US6410325-B1.
QY	420 RTHDHLCLDGGVKGKLIILQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHKSVM 479	XX 25-JUN-2002.
Db	453 RTHDHLCLDGGVKGKLIILQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHKSVM 512	XX 09-MAY-2001; 2001US-00851896.
QY	480 AYMRGMYFRMKDVFVGRSPYSGPLEEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPA 539	XX 09-MAY-2001; 2001US-00851896.
Db	513 AYMRGMYFRMKDVFVGRSPYSGPLEEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPA 572	PA (ISIS-) ISIS PHARM INC.
QY	540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRPNRFLDGG 599	XX Bennett CF, Freier SM, Watt AT;
Db	573 ELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRPNRFLDGG 632	XX WPI; 2002-616513/66.
QY	600 LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTRSPQVPTCVDFRPSNP 659	DR N-PSDB; AAD42941.

```
Db 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNVNQGTLPLHLACQLGQKQEMVRVLL 240
QY 241 LCNARCNTIMGPNGYPIHSAKFSQKGCAMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNTIMGPNGYPIHSAKFSQKGCAMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRGCVNSTSSAGNTALHVGWVRNRFDCAI VLLTHGANADARGEHGNTPHLAMSK 360
Db 301 RMLLKRGCVNSTSSAGNTALHVGWVRNRFDCAI VLLTHGANADARGEHGNTPHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGK-----LQDLMHISRARKPAFILGSMRDEKTHDHL 395
Db 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGRLVTRKAILTLRLTVGABYCFPPHIG 420
QY 396 -----LQDLMHISRARKPAFILGSMRDEKTHDHL 425
Db 421 VPAEQGSAAHPHFFSLERAQPPISLNLELQDLMHISRARKPAFILGSMRDEKTHDHL 480
QY 426 LCLDGGVKGKLIILQDLIAIEKASGVATKDLFDWAGTSTGGILALAILHLSKSMAYMRGM 485
Db 481 LCLDGGVKGKLIILQDLIAIEKASGVATKDLFDWAGTSTGGILALAILHLSKSMAYMRGM 540
QY 486 YFRMKDEVFRGSRPYESGPLEEFLEFKREFGEHTKMTDVRKPKVMLTGTLSDRQPAELHLFR 545
Db 541 YFRMKDEVFRGSRPYESGPLEEFLEFKREFGEHTKMTDVRKPKVMLTGTLSDRQPAELHLFR 600
QY 546 NYDAPETVREPRFNQNVNLRPPAQSDQLVRAARSSGAAPTYPFRPNRFLDGGLLANNP 605
Db 601 NYDAPETVREPRFNQNVNLRPPAQSDQLVRAARSSGAAPTYPFRPNRFLDGGLLANNP 660
QY 606 TLDAMTEIHEYNQDLIRKQANKVKLSIVSLGTGRSPQVPTCVDFRPSNPWELAKT 665
Db 661 TLDAMTEIHEYNQDLIRKQANKVKLSIVSLGTGRSPQVPTCVDFRPSNPWELAKT 720
QY 666 VFGAKELGKMVDDCCTDPDGR 686
Db 721 VFGAKELGKMVDDCCTDPDGR 741

RESULT 7
ADO19776
ID ADO19776 standard; protein; 806 AA.
AC ADO19776;
XX
XX
XX 12-AUG-2004 (first entry)
XX
XX Human PRO polypeptide #350.
XX
XX Human; PRO; immune related disorder; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
KW diabetes mellitus; renal disease; demyelinating disease;
KW central nervous system; peripheral nervous system;
KW demyelinating polyneuropathy; Guillain-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy.
XX
XX Homo sapiens.
XX
XX WO2004043361-A2.
XX
XX 27-MAY-2004.
XX
XX 06-NOV-2003; 2003WO-US035268.
XX
XX 08-NOV-2002; 2002US-0425235P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
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XX
DR N-PSDB; ADO19775.
XX
PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
PT treating an immune related disorder such as systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT spondyloarthritis.
XX
PS Claim 7; SEQ ID NO 700; 1731pp; English.
XX
XX The invention relates to human PRO polypeptides and the polynucleotides
XX encoding them. The polypeptides and polynucleotides are useful for
XX treating and diagnosing immune related disorders in mammals. The immune
XX related disorders include systemic lupus erythematosus, rheumatoid
XX arthritis, osteoarthritis, juvenile chronic arthritis, systemic
XX sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
XX haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
XX mellitus, immune-mediated renal disease, demyelinating diseases of the
XX central or peripheral nervous system, demyelinating polyneuropathy,
XX Guillain-Barre syndrome and chronic inflammatory demyelinating
XX polyneuropathy. This sequence represents a human PRO polypeptide of the
XX invention.
XX
XX Sequence 806 AA;
XX
XX Query Match 98.5%; Score 3566.5; DB 8; Length 806;
XX Best Local Similarity 92.3%; Pred. No. 0;
XX Matches 684; Conservative 1; Mismatches 1; Indels 55; Gaps 1;
QY 1 MQFGRLVNTSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MQFGRLVNTSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLFOLELEADALVNFHOYSQQLLPFYESSPQVLHTEVQLHLDLIRNHPSW 120
Db 61 NPNRSQSGFRLFOLELEADALVNFHOYSQQLLPFYESSPQVLHTEVQLHLDLIRNHPSW 120
QY 121 SVAHLAVELGIRECFPHHSRIISCANCAENEGCTPLHLACRKGDEILVELVOYCHTQMD 180
Db 121 SVAHLAVELGIRECFPHHSRIISCANCAENEGCTPLHLACRKGDEILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNVNQGTLPLHLACQLGQKQEMVRVLL 240
Db 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNVNQGTLPLHLACQLGQKQEMVRVLL 240
QY 241 LCNARCNTIMGPNGYPIHSAKFSQKGCAMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNTIMGPNGYPIHSAKFSQKGCAMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRGCVNSTSSAGNTALHVGWVRNRFDCAI VLLTHGANADARGEHGNTPHLAMSK 360
Db 301 RMLLKRGCVNSTSSAGNTALHVGWVRNRFDCAI VLLTHGANADARGEHGNTPHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGK-----LQDLMHISRARKPAFILGSMRDEKTHDHL 395
Db 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGRLVTRKAILTLRLTVGABYCFPPHIG 420
QY 396 -----LQDLMHISRARKPAFILGSMRDEKTHDHL 425
Db 421 VPAEQGSAAHPHFFSLERAQPPISLNLELQDLMHISRARKPAFILGSMRDEKTHDHL 480
QY 426 LCLDGGVKGKLIILQDLIAIEKASGVATKDLFDWAGTSTGGILALAILHLSKSMAYMRGM 485
Db 481 LCLDGGVKGKLIILQDLIAIEKASGVATKDLFDWAGTSTGGILALAILHLSKSMAYMRGM 540
QY 486 YFRMKDEVFRGSRPYESGPLEEFLEFKREFGEHTKMTDVRKPKVMLTGTLSDRQPAELHLFR 545
Db 541 YFRMKDEVFRGSRPYESGPLEEFLEFKREFGEHTKMTDVRKPKVMLTGTLSDRQPAELHLFR 600
QY 546 NYDAPETVREPRFNQNVNLRPPAQSDQLVRAARSSGAAPTYPFRPNRFLDGGLLANNP 605
Db 601 NYDAPETVREPRFNQNVNLRPPAQSDQLVRAARSSGAAPTYPFRPNRFLDGGLLANNP 660
```

QY 606 TLDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNPWELAKT 665
 Db 661 TLDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNPWELAKT 720
 QY 666 VFGAKELGKMWVDDCCTDPDGR 686
 Db 721 VFGAKELGKMWVDDCCTDPDGR 741

RESULT 8
 ABM84355
 ID ABM84355 standard; protein; 810 AA.
 AC ABM84355;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4604.
 XX
 KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
 XX
 OS Homo sapiens.
 XX
 PN WO2004023973-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 12-SEP-2003; 2003WO-US028227.
 XX
 PR 12-SEP-2002; 2002US-0410259P.
 XX
 PR 12-SEP-2002; 2002US-0410260P.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
 PI Mooney EM, Deleagane AM, Panesar IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patury S, Shi X, Suarez CJ;
 XX
 WPI; 2004-329368/30.
 DR N-PSDB; ACN43007.
 XX
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX
 PS Claim 27; Page; 190pp; English.
 XX
 CC The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX
 SQ Sequence 810 AA;

Query Match 97.9%; Score 3544.5; DB 8; Length 810;
 Best Local Similarity 91.8%; Pred. No. 0;
 Matches 684; Conservative 1; Mismatches 1; Indels 59; Gaps 3;
 QY 1 MOFFGRLVNTFSQVNTLFSNPRFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
 Db 1 MOFFGRLVNTFSQVNTLFSNPRFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
 QY 61 NPRNSQSGFRLFQLELEADALVNFHOYSQQLLPFFYESSQVLHTEVLOHLTDLIRNHPSW 120
 Db 61 NPRNSQSGFRLFQLELEADALVNFHOYSQQLLPFFYESSQVLHTEVLOHLTDLIRNHPSW 120
 QY 121 SVAHLAVELGIRECFHHSRII-----SCANCAENE 152
 Db 121 SVAHLAVELGIRECFHHSRIIIRVRSAHQVPGWLWELISTHEIEFFSPPXSCANCAENE 180
 QY 153 CTPLHLACRKGDEILVELVQYCHTQMDVTDYKGETVFHYAVQGDNSQVLQLGRNAVAG 212
 Db 181 CTPLHLACRKGDEILVELVQYCHTQMDVTDYKGETVFHYAVQGDNSQVLQLGRNAVAG 240
 QY 213 LNOVNNQGLTPLHLACQLGKQEMVRVLLLCNARCNTIMGPNGYPIHSAMKFSQKGCAMII 272
 Db 241 LNOVNNQGLTPLHLACQLGKQEMVRVLLLCNARCNTIMGPNGYPIHSAMKFSQKGCAMII 300
 QY 273 SMDSSQIHSKDPYRGASPLHWAKNAEMARMILLKRCNCNVNSTSSAGNTALHVGVMRNRFC 332
 Db 301 SMDSSQIHSKDPYRGASPLHWAKNAEMARMILLKRCNCNVNSTSSAGNTALHVGVMRNRFC 360
 QY 333 AIVLLTHGANADARGEHNTPLHLAMS KDNVEMI KALIVFGAEVDTPNDFGETPTFLASK 392
 Db 361 AIVLLTHGANADARGEHNTPLHLAMS KDNVEMI KALIVFGAEVDTPNDFGETPTFLASK 420
 QY 393 ICK-LQDLMIHSRARKPAFIFLSMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGV 451
 Db 421 ICK-LQDLMIHSRARKPAFIFLSMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGV 480
 QY 452 ATKOLFDMWAGTSTGGILALAILHSKSMAYMRGMFRMKDEVRGSRPYESGPLEFLKR 511
 Db 481 ATKOLFDMWAGTSTGGILALAILHSKSMAYMRGMFRMKDEVRGSRPYESGPLEFLKR 540
 QY 512 EFGETKMTDVRKPK-----VMLTGTLSDRPAEL 541
 Db 541 EFGETKMTDVRKPKLDQSDTPPALPERACFAGWVRGEAHLSETVMLTGTLSDRPAEL 600
 QY 542 HLFNRYDAPETVREPRFNQNVNLRPPAQPSDQLWRAARSSGAAPTYFRPNRFLDGLL 601
 Db 601 HLFNRYDAPETVREPRFNQNVNLRPPAQPSDQLWRAARSSGAAPTYFRPNRFLDGLL 660
 QY 602 ANNPILDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNPWE 661
 Db 661 ANNPILDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNPWE 720
 QY 662 LAKTVFGAKELGKMWVDDCCTDPDGR 686
 Db 721 LAKTVFGAKELGKMWVDDCCTDPDGR 745

RESULT 9
 ABM84354
 ID ABM84354 standard; protein; 810 AA.
 XX
 AC ABM84354;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4603.
 XX
 KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
 XX
 OS Homo sapiens.
 XX
 PN WO2004023973-A2.
 XX

CC e.g. rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease
CC and other disease mediated by increased levels of prostaglandins,
CC leukotriene or platelet activating factor. The enzyme can also be used
XX for the production of antibodies for use as research or diagnostic tools
SQ Sequence 752 AA;

Query Match 91.2%; Score 3302.5; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MQFFGLVNTFSGVTNLFNSNPFVKVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGLVNTLSSVTNLFNSNPFVKVAVADYTSDDRVREEGQLILFQNTPNRTWDCILV 60
QY 61 NPNRSQSGFRLFOLEADALVNFHQSOLLPPFYESSQVLTHTVQLHLDLIRNHPWS 120
Db 61 SPRNPHSGFRLFOLEADALVNFHQSOLLPPFYESSQVLTHTVQLHLDLIRNHPWS 120
QY 121 SVAVHVELGIRECFHHSRIISCANCAENEBCGCTPLHLACRKGDSILVELVQYCHTQMD 180
Db 121 TVTHLVELGIRECFHHSRIISCANSTENEGCTPLHLACRKGDSILVELVQYCHQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLTGKNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDNKGETAFHYAVQGDNSQVLTGKNAVAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
QY 241 LCNARCNINMGPNQYPIHSAKMSQKCAEMIISMDSSQIHSDKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNVMPGSPGFPHTAMKFSQKCAEMIISMDSSQIHSDKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLKGCVDVSTSAAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAISK 360
QY 361 DNVEIMKALIVFGAEVDTNDPGETTFLASKIGK-LQDLMHISRARKPAFILGSRMRDEK 419
Db 361 DNMEMIKALIVFGAEVDTNDPGETTFLASKIGK-LQDLMHISRARKPAFILGSRMRDEK 420
QY 420 RTHDHLCLDGGVKGKLIILQLLIAIEKASGVATKOLFQWVAGTSTGGILALAILHSKSM 479
Db 421 RTHDHLCLDGGVKGKLIILQLLIAIEKASGVATKOLFQWVAGTSTGGILALAILHSKSM 480
QY 480 AYMRGMVFMKDEVRFGSPYSGPLLEFLKRFEGEHTKMTDVRKPKVMLTGTLSRQPA 539
Db 481 AYMRGVYFMKDEVRFGSPYSGPLLEFLKRFEGEHTKMTDVRKPKVMLTGTLSRQPA 540
QY 540 ELHLFRNYDAPETVREPRNQNLAPPQPSQVLAARSSGAAPTFRPNRGLDGG 599
Db 541 ELHLFRNYDAPETVREPRNQNLAPPQPSQVLAARSSGAAPTFRPNRGLDGG 600
QY 600 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNP 659
Db 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNP 660
QY 660 WELAKTVFGAKELGKMWVDCCTDPDGR 686
Db 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 11
AAW01479
ID AAW01479 standard; protein; 752 AA.
XX
AC AAW01479;
XX
XX
DT 25-MAR-2003 (revised)
DT 12-FEB-1997 (first entry)
DE
DE
XX Calcium-independent cytosolic phospholipase A2/B.
XX cPLA2/B; calcium-independent cytosolic phospholipase A2/B;
KW arachidonic acid; 1-palmitoyl-2-[14C]-arachidonyl-phosphatidylcholine;

anti-inflammatory; screen; rheumatoid arthritis.
Synthetic.
US5554511-A.
XX
XX 10-SEP-1996.
XX
PF 14-APR-1995; 95US-00422420.
XX
XX 27-JUL-1994; 94US-00281193.
XX
(GEMY) GENETICS INST INC.
XX
XX Tang J, Jones S;
XX
XX WPI; 1996-424653/42.
XX
XX N-PSDB; AAT44578.
XX
PT Prodn. of a Ca-independent cytosolic phospholipase A(2)/B - by culturing
PT host cells contg. the phospholipase gene, useful for screening anti-
PT inflammatory agents for treating e.g. rheumatoid arthritis.
XX
PS Claim 1; Col 15-22; 24pp; English.
XX
XX The present sequence is that of a calcium-independent cytosolic
XX phospholipase A2/B (cPLA2/B) enzyme. cPLA2/B is important in the release
XX of arachidonic acid in specific tissues characterised by unique membrane
XX phospholipids. The invention provides a process for producing such an
XX enzyme. The enzyme has a mol. wt. of 86 kD on SDS-PAGE and the presence
XX of one or more amino acid sequences selected from AAW01480-92; cPLA2/B
XX has activity in a mixed micelle assay with 1-palmitoyl-2-[14C]-
XX arachidonyl-phosphatidylcholine. The enzyme is useful for screening anti-
XX inflammatory agents mediated by the arachidonic acid cascade, for
XX treating, e.g. rheumatoid arthritis (Updated on 25-MAR-2003 to correct PF
XX field.)
SQ Sequence 752 AA;

Query Match 91.2%; Score 3302.5; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MQFFGLVNTFSGVTNLFNSNPFVKVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGLVNTLSSVTNLFNSNPFVKVAVADYTSDDRVREEGQLILFQNTPNRTWDCILV 60
QY 61 NPNRSQSGFRLFOLEADALVNFHQSOLLPPFYESSQVLTHTVQLHLDLIRNHPWS 120
Db 61 SPRNPHSGFRLFOLEADALVNFHQSOLLPPFYESSQVLTHTVQLHLDLIRNHPWS 120
QY 121 SVAVHVELGIRECFHHSRIISCANCAENEBCGCTPLHLACRKGDSILVELVQYCHTQMD 180
Db 121 TVTHLVELGIRECFHHSRIISCANSTENEGCTPLHLACRKGDSILVELVQYCHQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLTGKNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDNKGETAFHYAVQGDNSQVLTGKNAVAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
QY 241 LCNARCNINMGPNQYPIHSAKMSQKCAEMIISMDSSQIHSDKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNVMPGSPGFPHTAMKFSQKCAEMIISMDSSQIHSDKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLKGCVDVSTSAAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAISK 360
QY 361 DNVEIMKALIVFGAEVDTNDPGETTFLASKIGK-LQDLMHISRARKPAFILGSRMRDEK 419
Db 361 DNMEMIKALIVFGAEVDTNDPGETTFLASKIGK-LQDLMHISRARKPAFILGSRMRDEK 420
QY 420 RTHDHLCLDGGVKGKLIILQLLIAIEKASGVATKOLFQWVAGTSTGGILALAILHSKSM 479

Db 421 RIHDLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480
 QY 480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLEKREFGHEHTKMTDVRKPKVMTGTLSDRQPA 539
 Db 481 AYMRGVYFRMKDEVFRGSRPYESGPLEEFLEKREFGHEHTKMTDVRKPKVMTGTLSDRQPA 540
 QY 540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFFRNGRFLDGG 599
 Db 541 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFFRNGRFLDGG 600
 QY 600 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
 Db 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
 QY 660 WELAKTVFGAKELGKMWVDDCCTDPDGR 686
 Db 661 WELAKTVFGAKELGKMWVDDCCTDPDGR 687

RESULT 12
 AAW13163
 ID AAW13163 standard; protein; 752 AA.
 XX
 AC AAW13163;
 XX
 DT 17-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 20-MAY-1997 (first entry)
 XX
 XX Ca-independent phospholipase A2/B protein.
 DE
 KW Ca-independent phospholipase A2/B; Chinese hamster ovary cell; probe;
 KW chromatography; DEAE anion exchange; hydrophobic interaction; lambda;
 KW heparin Toyopearl; chromatofocusing; eukaryotic expression vector; COS;
 KW CHO; inhibitor; anti-inflammatory agent; arachidonic acid cascade.
 XX
 OS Cricetulus griseus; ovary cells.
 PN US5589170-A.
 XX
 PD 31-DEC-1996.
 XX
 PF 14-APR-1995; 95US-00422106.
 XX
 PR 27-JUL-1994; 94US-00281193.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Tang J, Jones S;
 XX
 DR WPI: 1997-076789/07.
 DR N-PSDB; AAT59199.
 XX
 PT Compon. comprising calcium-independent phospholipase enzyme - for
 PT screening for anti-inflammatory agents.
 XX
 PS Claim 5; Col 15-22; 24pp; English.
 XX
 CC This is the amino acid sequence of the Ca-independent phospholipase A2/B
 CC from Chinese hamster ovary cells. The protein was isolated from these
 CC cells by conventional chromatographic methods e.g. DEAE anion exchange,
 CC hydrophobic interaction, heparin Toyopearl and Mono P 5/20
 CC chromatofocusing chromatography. The purified protein has mol. wt. of 86
 CC kD and an optimum pH 6. The protein was used for amino acid sequencing
 CC from which pools of degenerate probes were synthesised. The probes were
 CC used to screen a CHO cell cDNA library in lambda ZAPII vector. Of 40000
 CC recombinant phages screened, 12 positive plaques were isolated. One of
 CC these, designated clone 9, contained this sequence. The phospholipase
 CC gene can be inserted into eukaryotic vectors for expression in COS or CHO
 CC cells. The protein, or peptides derived from it e.g. AAW13164-76, can be
 CC used to identify phospholipase inhibitors that can be used as anti-
 CC inflammatory agents, esp. against components of the arachidonic acid
 CC cascade. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT

CC -2003 to standardise OS field)
 XX
 SQ Sequence 752 AA;
 Query Match 91.2%; Score 3302.5; DB 2; Length 752;
 Best Local Similarity 90.4%; Pred. No. 0;
 Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;
 QY 1 MQFFGRLVNTSGVNTLFSNPRVKEVAVADVTSSDRVREEGQLILFQNTPNRTWDCVILV 60
 Db 1 MQFFGRLVNTLSSVNTLFSNPRVKEISVADVTSHRVREEGQLILFQNASRNTWDCILV 60
 QY 61 NPNRSQSQFRLFQLEADALVNFHQYSSQLLPFYESSPQVLHTEVQLHQLTLIRNHPSW 120
 Db 61 SPRNPHSGFRLFQLESEADALVNFQFSSQLPPFYESSVQVLHVEVQLHLSDLIRSHPSW 120
 QY 121 SVAHLAVELGIRECFPHHSRIISCANCAENEGECTPLHLACRKGDEIIVELVOYCHTQMD 180
 Db 121 TVTHLAVELGIRECFPHHSRIISCANSTENEGECTPLHLACRKGDSIIVELVOYCHAQMD 180
 QY 181 VTDYKGETVEHYAVOGDINSQVLLGLGRNAVAGLNQVNOGLTPLHLACOLGKQEMVRVLL 240
 Db 181 VTDNKGETAHYAVOGDINSQVLLGLGKNASAGLNQVNOGLTPLHLACOMGQEMVRVLL 240
 QY 241 LCNARCNTMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSXDPYRGASPLHWAKNAEMA 300
 Db 241 LCNARCNVMPGSGPPIHTAMKFSQKCAEMIISMDSQIHSXDPYRGASPLHWAKNAEMA 300
 QY 301 RMLLRGCVNVSSTAGNTALHVGVMRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
 Db 301 RMLLRGCDVDSTSAAGNTALHVAVMRNFDCVMVLLTYGANAGTPEGHNTPLHLAISK 360
 QY 361 DNEMIKALIIVFGAEVDPNDPGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 419
 Db 361 DNEMIKALIIVFGAEVDPNDPGETPTAFMAKISKISQLQDLMPISARARKPAFILGSMRDEK 420
 QY 420 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 479
 Db 421 RIHDLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480
 QY 480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLEKREFGHEHTKMTDVRKPKVMTGTLSDRQPA 539
 Db 481 AYMRGVYFRMKDEVFRGSRPYESGPLEEFLEKREFGHEHTKMTDVRKPKVMTGTLSDRQPA 540
 QY 540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFFRNGRFLDGG 599
 Db 541 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFFRNGRFLDGG 600
 QY 600 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
 Db 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
 QY 660 WELAKTVFGAKELGKMWVDDCCTDPDGR 686
 Db 661 WELAKTVFGAKELGKMWVDDCCTDPDGR 687

RESULT 13
 AAW17849
 ID AAW17849 standard; protein; 752 AA.
 XX
 AC AAW17849;
 XX
 DT 27-AUG-2003 (revised)
 DT 07-AUG-1997 (first entry)
 XX
 DE Hamster cytosolic phospholipase A2/B.
 KW Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
 KW inflammation; inhibitor; antiinflammatory; CHO.
 XX
 OS Cricetus.
 XX

Key	Location/Qualifiers	Active-site	465	note= "mutagenesis of Ser-465 results in loss of activity"
W09717448-A2.				
15-MAY-1997.				
07-NOV-1996;	96WO-US017794.			
08-NOV-1995;	95US-00555568.			
(GEMY) GENETICS INST INC.				
Jones S, Tang J;				
WPI; 1997-281037/25.				
N-PSDB; AA768827.				
Calcium independent phospholipase A2/B - used to reduce inflammation in a mammalian subject.				
Example 4; Page 33-36; 74pp; English.				
A novel hamster cytosolic phospholipase A2/B (sPLA2/B) (AAW17849) is thought to be involved in the arachidonic acid cascade. Its amino acid sequence was deduced from a cDNA clone (AA768827) obcd. from a CHO-DUX cDNA library. The recombinant enzyme has been expressed in CHO and COS host cells. Human sPLA2/B polypeptides (see also AAW17845-48) have also been isolated. These can be used to screen for inhibitors useful as antiinflammatory agents that block the arachidonic acid cascade in mammals. (Updated on 27-AUG-2003 to correct OS field.)				
Sequence 752 AA;				
Query Match	91.2%;	Score 3302.5;	DB 2;	Length 752;
Best Local Similarity	90.4%;	Pred. No. 0;		
Matches 621;	Conservative 31;	Mismatches 34;	Indels 1;	Gaps 1;
QY	1	MOFFGRVNTFSVNTLSPNPRVKEVAVADYTSDDRVRESGQLILFQNTNRTWDCVLV	60	
DB	1	MOFFGRVNTLSSVNTLSPNPRVKEISVADYTSHERVREEGQLILFQNASNRTWDCILV	60	
QY	61	NPRNSQSGRLFQLEADALVNFHQYSQQLLPFYESSPQVLHTEVLQHLTDLIRNHPWS	120	
DB	61	SPRNPHSGRLFQLESEADALVNFQFSSQLPPFYESSQVLHVEVLQHLSDLIRSHPSW	120	
QY	121	SVAHAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEILVELVQYCHTQMD	180	
DB	121	TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRKGDEILVELVQYCHAQMD	180	
QY	181	VTDYKGETVHYAVQDINSQVLIILGRNAVAGLNQVNOGLTPLHLACQLGKQEMVRVLL	240	
DB	181	VTDNKGETAHYAVQDINSQVLIILGRNAVAGLNQVNOGLTPLHLACQMGKQEMVRVLL	240	
QY	241	LCNARCINMGPGYPTHSAMKSGKQCAEMIISMDSSQIHSKDPYRGASPLHWAQNAEMA	300	
DB	241	LCNARCINMGPGFPDTHAMKSGKQCAEMIISMDSSQIHSKDPYRGASPLHWAQNAEMA	300	
QY	301	RMLLKRGCVNNTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK	360	
DB	301	RMLLKRGCDVSTSAAGNTALHVAVMNRNFDCAIVLLTYGANAGTPGEGHNTPLHLAISK	360	
QY	361	DNVEMIKALIVGAEDVTDNDPGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK	419	
DB	361	DNMEMIKALIVGAEDVTDNDPGETPTAFMASKISKQLQDLMIPISRARKPAFILSSMRDEK	420	
QY	420	RYTHDLLCLDGGVGKGLIIQLIIAIEKASGVATKDLFDWAGTSTGGILALATLHKSMM	479	
DB	421	RIHDDLCLDGGVGKGLVIIQLIIAIEKASGVATKDLFDWAGTSTGGILALATLHKSMM	480	
QY	480	AYMRGMVFRMKDEVFRGSRPYESGLEEFLEKREFEHNTKMTDVRKPKVMTLGTLSDRQPA	539	

XX US2002106364-A1.
 PN 08-AUG-2002.
 PD 09-AUG-2001; 2001US-00927180.
 XX 27-JUL-1994; 94US-00281193.
 PR 14-APR-1995; 95US-00422106.
 PR 14-APR-1995; 95US-00422420.
 PR 26-JUN-1995; 95WO-US008069.
 PR 08-NOV-1995; 95US-00555568.
 PR 09-SEP-1998; 98US-00149988.
 PR 06-MAR-2000; 2000US-00519223.
 XX (GEMY) GENETICS INST INC.
 PA Jones S, Tang J;
 XX WPI; 2002-739923/80.
 DR N-PSDB; ABV73011.
 XX Novel composition comprising purified mammalian calcium independent phospholipase enzyme, useful for the screening of inhibitors of phospholipase activity, is active in the absence of calcium.
 PT Claim 6; Page 28-30; 4lpp; English.
 XX The invention relates to a purified mammalian calcium independent cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is characterized by activity in the absence of calcium and has a molecular weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified calcium independent phospholipase enzyme is useful for identifying an inhibitor of phospholipase activity which involves combining (I), phospholipid and candidate inhibitor compound, and observing whether the enzyme cleaves the phospholipid and releases fatty acid from it. A pharmaceutical composition (PC) comprising a therapeutically effective amount of the inhibitor is useful for reducing inflammation and for treating inflammatory conditions including rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease and other diseases mediated by increased levels of prostaglandins, leukotriene or platelet activating factor. A composition comprising an antibody which binds to (I) is useful as research and diagnostic tool, and is also useful in the study of phospholipase A2 activity and inflammatory conditions. The present sequence represents a human cPLA2/B enzyme longer splice variant (clone 19b)
 CC Sequence 688 AA;
 SQ
 Query Match 99.6%; Score 3606.5; DB 5; Length 688;
 Best Local Similarity 99.7%; Pred. NO. 0;
 Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MOFFGLVNTFSGVTLNFSNPRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
 DB 1 MOFFGLVNTFSGVTLNFSNPRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
 QY 61 NPNRSQSGFRLFQLEADALVNFHOYSQQLPFYESSQVHLTEVQLHLDLIRNHPSW 120
 DB 61 NPNRSQSGFRLFQLEADALVNFHOYSQQLPFYESSQVHLTEVQLHLDLIRNHPSW 120
 QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDBGILVELVOYCHTQMD 180
 DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDBGILVELVOYCHTQMD 180
 QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLQVNNQGLTPLHLACOLGQEMVRVLL 240
 DB 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLQVNNQGLTPLHLACOLGQEMVRVLL 240
 QY 241 LCNARCINMGPNGYPIHSAKMSQKCAEWIISMDSSQIHSDKDPYGCASPLHWAKNAEMA 300
 DB 241 LCNARCINMGPNGYPIHSAKMSQKCAEWIISMDSSQIHSDKDPYGCASPLHWAKNAEMA 300

QY 301 RMLLKRGCVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
 DB 301 RMLLKRGCVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
 QY 361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIGK-LODLMIHSRARKPAFTLGSNRDEK 419
 DB 361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIGKLODLMIHSRARKPAFTLGSNRDEK 420
 QY 420 RTHDHLCLDGGGVKGLIIIIQLLIAEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 479
 DB 421 RTHDHLCLDGGGVKGLIIIIQLLIAEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480
 QY 480 AYMRGMYFRMKDEVPGRSGRPYESGLEEFLEKEFEHKTMDVRPKVMTCTLSDRQPA 539
 DB 481 AYMRGMYFRMKDEVPGRSGRPYESGLEEFLEKEFEHKTMDVRPKVMTCTLSDRQPA 540
 QY 540 ELHLFRNYDAPETVREPRFNQNVNLRPPAQSDQLVWRAARSSGAAPTFFRNGRFLDGG 599
 DB 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQSDQLVWRAARSSGAAPTFFRNGRFLDGG 600
 QY 600 LLANNPTLDAMTEIHEYNOQLIRKGOANKVKLSIVVSLGTGRSPQVPVTCVDFRPSNP 659
 DB 601 LLANNPTLDAMTEIHEYNOQLIRKGOANKVKLSIVVSLGTGRSPQVPVTCVDFRPSNP 660
 QY 660 WELAKTVFGAKELGKMVVDCTDPPGRP 687
 DB 661 WELAKTVFGAKELGKMVVDCTDPPGRP 688
 RESULT 5
 ADD93407
 ID ADD93407 standard; protein; 784 AA.
 XX AC ADD93407;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human lipid-associated molecule LIPAM-14 polypeptide.
 XX Human; lipid-associated molecule; LIPAM-14; neuroprotective; relaxant;
 KW antithyroid; antidiabetic; cytostatic; dermatological; immunosuppressive;
 KW antiinflammatory; thyromimetic; antiallergic; cerebroprotective;
 KW gastrointestinal; hepatotropic; nephrotropic; anticonvulsant;
 KW antiparkinsonian; antibacterial; antiparasitic; fungicide; protozoacide;
 KW virucide; uropathic; antirheumatic; cardiant; cardiovascular; anti-HIV;
 KW nootropic.
 XX OS Homo sapiens.
 XX PN WO2003083081-A2.
 XX PD 09-OCT-2003.
 XX PF 27-MAR-2003; 2003WO-US009755.
 XX PR 29-MAR-2002; 2002US-0368722P.
 PR 03-MAY-2002; 2002US-0377576P.
 PR 05-JUL-2002; 2002US-0393934P.
 PR 27-SEP-2002; 2002US-0414269P.
 XX (INCY-) INCYTE CORP.
 XX Emerling BM, Marquis JP, Chawla NK, Lee SY, Duggan BM, Warren BA;
 PI Baughn MR, Lee EA, Griffin JA, Kable AE, Elliott VS, Chang H;
 PI Lee S, Ramkumar J, Bulloch SA, Hatalia AJA, Khare R, Jiang X;
 PI Jackson AA;
 XX WPI; 2003-788347/74.
 DR N-PSDB; ADD93426.
 XX New LIPAM polypeptides, useful for diagnosing, preventing, and treating
 PT disorders associated with abnormal expression or activity of LIPAM, e.g.
 PT neuromuscular, immunological, cardiovascular disorders, cancer and/or

Db 301 RMLLKRCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHGNTPHLAMSK 360
 QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGKQLQDLMHISRARKPAFILGSMRDEKR 420
 Db 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGKQLQDLMHISRARKPAFILGSMRDEKR 420
 QY 421 THDHLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMA 480
 Db 421 THDHLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMA 480
 QY 481 YMRGMYFRMKDEVRGSRPYESGPLEEFLEKREFGEHTKMDVRKPKVMTLGTLSDRQPAE 540
 Db 481 YMRGMYFRMKDEVRGSRPYESGPLEEFLEKREFGEHTKMDVRKPKVMTLGTLSDRQPAE 540
 QY 541 LHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRAARSSGAAPTYPFRPNGRFLDGG 600
 Db 541 LHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRAARSSGAAPTYPFRPNGRFLDGG 600
 QY 601 LANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNPW 660
 Db 601 LANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNPW 660
 QY 661 ELAKTVFGAKELGKMVDDCCTDPGRP 687
 Db 661 ELAKTVFGAKELGKMVDDCCTDPGRP 687

RESULT 3
 AAW17848
 ID AAW17848 standard; protein; 688 AA.
 AC AAW17848;
 DT 07-AUG-1997 (first entry)
 XX Cytosolic phospholipase A2/B (alternatively spliced clone 19b).
 DE Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
 KW inflammation; inhibitor; antiinflammatory.
 XX Homo sapiens.
 XX WO9717448-A2.
 PN 15-MAY-1997.
 PD
 XX 07-NOV-1996; 96WO-US017794.
 PF
 XX 08-NOV-1995; 95US-00555568.
 PR (GEMY) GENETICS INST INC.
 XX Jones S, Tang J;
 PI WPI; 1997-281037/25.
 DR N-PSDB; AAT68826.
 XX
 PT Calcium independent phospholipase A2/B - used to reduce inflammation in a mammalian subject.
 XX
 PS Claim 12; Page 54-56; 74pp; English.
 CC A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17848) is characterised by activity in the absence of calcium, by activity in a mixed micelle assay with 1-palmitoyl-2-(14C) - arachidonyl-phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a lack of stimulation by ATP, and by including in its sequence at least one of the amino acid sequences given in AAW17839-44). It is an alternatively spliced variant of another isolated polypeptide (AAW17846) and is encoded by an isolated cDNA (AAT68826). Other PLA2/B enzymes (AAW17845, AAW17847) have also been identified. sPLA2/B enzymes are thought to be involved in the release of arachidonic acid in specific tissues. Recombinant sPLA2/B polypeptides produced in transformed host

CC cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory drugs which inhibit the arachidonic acid cascade
 XX
 SQ Sequence 688 AA;
 Query Match 99.6%; Score 3606.5; DB 2; Length 688;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MOFFGRLVNTFSGVNTLFSNPRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
 Db 1 MOFFGRLVNTFSGVNTLFSNPRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
 QY 61 NPNRSOSGFRLLFQLELEADALVNFHOYSQQLPFFYESSQVLTHTVQLHTLTLIRHPSW 120
 Db 61 NPNRSOSGFRLLFQLELEADALVNFHOYSQQLPFFYESSQVLTHTVQLHTLTLIRHPSW 120
 QY 121 SVAHLAVELGIRECFPHHSRIISCANCAENEBCGCTPLHLACRKGDEILVELVQYCHTQMD 180
 Db 121 SVAHLAVELGIRECFPHHSRIISCANCAENEBCGCTPLHLACRKGDEILVELVQYCHTQMD 180
 QY 181 VTDYKGETVFHYAVQGDNSQVLLQGLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
 Db 181 VTDYKGETVFHYAVQGDNSQVLLQGLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
 QY 241 LCNARCNIIMPNGYPITHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHWAKNAEMA 300
 Db 241 LCNARCNIIMPNGYPITHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHWAKNAEMA 300
 QY 301 RMLLKRCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHGNTPHLAMSK 360
 Db 301 RMLLKRCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHGNTPHLAMSK 360
 QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMHISRARKPAFILGSMRDEK 419
 Db 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMHISRARKPAFILGSMRDEK 420
 QY 420 RTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMA 479
 Db 420 RTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMA 480
 QY 480 AYMRGMYFRMKDEVRGSRPYESGPLEEFLEKREFGEHTKMDVRKPKVMTLGTLSDRQPA 539
 Db 480 AYMRGMYFRMKDEVRGSRPYESGPLEEFLEKREFGEHTKMDVRKPKVMTLGTLSDRQPA 540
 QY 540 ELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRAARSSGAAPTYPFRPNGRFLDGG 599
 Db 540 ELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRAARSSGAAPTYPFRPNGRFLDGG 600
 QY 600 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
 Db 600 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
 QY 660 WELAKTVFGAKELGKMVDDCCTDPGRP 687
 Db 660 WELAKTVFGAKELGKMVDDCCTDPGRP 688

RESULT 4
 ABB82232
 ID ABB82232 standard; protein; 688 AA.
 AC ABB82232;
 XX
 XX 08-JAN-2003 (first entry)
 DT Human cPLA2/B splice variant (clone 19b).
 DE
 XX Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
 KW antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;
 XX antiasthmatic; human.
 OS Homo sapiens.

XX	PD	XX	08-AUG-2002.
XX	XX	XX	09-AUG-2001; 2001US-00927180.
XX	XX	XX	27-JUL-1994; 94US-00281193.
XX	XX	XX	14-APR-1995; 95US-00422106.
XX	XX	XX	14-APR-1995; 95US-00422106.
XX	XX	XX	26-JUN-1995; 95WO-US008069.
XX	XX	XX	08-NOV-1995; 95US-00555568.
XX	XX	XX	09-SEP-1998; 98US-00149988.
XX	XX	XX	06-MAR-2000; 2000US-00519223.
XX	XX	XX	(GEMY) GENETICS INST INC.
XX	XX	XX	Jones S, Tang J;
XX	XX	XX	WPI: 2002-739923/80.
XX	XX	XX	N-PSDB; ABV73010.
XX	XX	XX	Novel composition comprising purified mammalian calcium independent phospholipase enzyme, useful for the screening of inhibitors of phospholipase activity, is active in the absence of calcium.
XX	XX	XX	Claim 6; Page 23-25; 41pp; English.
XX	XX	XX	The invention relates to a purified mammalian calcium independent cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is characterized by activity in the absence of calcium and has a molecular weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified calcium independent phospholipase enzyme is useful for identifying an inhibitor of phospholipase activity which involves combining (I), phospholipid and candidate inhibitor compound, and observing whether the enzyme cleaves the phospholipid and releases fatty acid from it. A pharmaceutical composition (PC) comprising a therapeutically effective amount of the inhibitor is useful for reducing inflammation and for treating inflammatory conditions including rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease and other diseases mediated by increased levels of prostaglandins, leukotriene or platelet activating factor. A composition comprising an antibody which binds to (I) is useful as research and diagnostic tool, and is also useful in the study of phospholipase A2 activity and inflammatory conditions. The present sequence represents a human cPLA2/B enzyme longer splice variant (clone 19a)
XX	XX	XX	Query Match 100.0%; Score 3620; DB 5; Length 687; Best Local Similarity 100.0%; Pred. No. 0; Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	XX	XX	1 MOFFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
XX	XX	XX	1 MOFFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
XX	XX	XX	61 NPNRSQSGFRLFQLEADALVNFHQSOLLPPFYESSPQVLHTEVQLHLDLIRNHPW 120
XX	XX	XX	61 NPNRSQSGFRLFQLEADALVNFHQSOLLPPFYESSPQVLHTEVQLHLDLIRNHPW 120
XX	XX	XX	121 SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEILVELVQYCHTQMD 180
XX	XX	XX	121 SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEILVELVQYCHTQMD 180
XX	XX	XX	181 VTDYKGETVFHYAVOGDNSQVLQLGRNAVAGLVNNOGLTPLHLACOLGQEMVRVLL 240
XX	XX	XX	181 VTDYKGETVFHYAVOGDNSQVLQLGRNAVAGLVNNOGLTPLHLACOLGQEMVRVLL 240
XX	XX	XX	241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYKASPLHAKNAEMA 300
XX	XX	XX	241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYKASPLHAKNAEMA 300
XX	XX	XX	301 RMLLKRCGNVNTSSAGNTALHVGVRNRFDCAIIVLLTHGANADARGHGNTPLHLAMSK 360
XX	XX	XX	Query Match 100.0%; Score 3620; DB 2; Length 687; Best Local Similarity 100.0%; Pred. No. 0; Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	XX	XX	1 MOFFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
XX	XX	XX	1 MOFFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
XX	XX	XX	61 NPNRSQSGFRLFQLEADALVNFHQSOLLPPFYESSPQVLHTEVQLHLDLIRNHPW 120
XX	XX	XX	61 NPNRSQSGFRLFQLEADALVNFHQSOLLPPFYESSPQVLHTEVQLHLDLIRNHPW 120
XX	XX	XX	121 SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEILVELVQYCHTQMD 180
XX	XX	XX	121 SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEILVELVQYCHTQMD 180
XX	XX	XX	181 VTDYKGETVFHYAVOGDNSQVLQLGRNAVAGLVNNOGLTPLHLACOLGQEMVRVLL 240
XX	XX	XX	181 VTDYKGETVFHYAVOGDNSQVLQLGRNAVAGLVNNOGLTPLHLACOLGQEMVRVLL 240
XX	XX	XX	241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYKASPLHAKNAEMA 300
XX	XX	XX	241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYKASPLHAKNAEMA 300
XX	XX	XX	301 RMLLKRCGNVNTSSAGNTALHVGVRNRFDCAIIVLLTHGANADARGHGNTPLHLAMSK 360
XX	XX	XX	301 RMLLKRCGNVNTSSAGNTALHVGVRNRFDCAIIVLLTHGANADARGHGNTPLHLAMSK 360
XX	XX	XX	361 DNVEIMKALIVGAEDVTPNDPGETPTFLASKIGKLQDLMIHSRARKPAFILGSMRDEKR 420
XX	XX	XX	361 DNVEIMKALIVGAEDVTPNDPGETPTFLASKIGKLQDLMIHSRARKPAFILGSMRDEKR 420
XX	XX	XX	421 THDHLCLDGGVGKGLIIQLLITAIKASGVATKDLFDWAGTSTGGTILAILHSKMA 480
XX	XX	XX	421 THDHLCLDGGVGKGLIIQLLITAIKASGVATKDLFDWAGTSTGGTILAILHSKMA 480
XX	XX	XX	481 YMRGMVPMKDEVFRSGRPSYSGPLEEFKRFEGHTKMTDVRKPKWMLTGTLSDRQPAE 540
XX	XX	XX	481 YMRGMVPMKDEVFRSGRPSYSGPLEEFKRFEGHTKMTDVRKPKWMLTGTLSDRQPAE 540
XX	XX	XX	541 LHLFRNYDAPETVREPRFNQNVNLRPPAQPSPDLVRAARSSGAAPTFRPNRFLDGLL 600
XX	XX	XX	541 LHLFRNYDAPETVREPRFNQNVNLRPPAQPSPDLVRAARSSGAAPTFRPNRFLDGLL 600
XX	XX	XX	601 LANNPTLDAMTEHEYNODLIRGQANKYKLSIVVSLGTGRSPQVPTCDVFRPSNPW 660
XX	XX	XX	601 LANNPTLDAMTEHEYNODLIRGQANKYKLSIVVSLGTGRSPQVPTCDVFRPSNPW 660
XX	XX	XX	661 ELAKTVFGAKELGKVVVDCCTDPPGR 687
XX	XX	XX	661 ELAKTVFGAKELGKVVVDCCTDPPGR 687
XX	XX	XX	RESULT 2
XX	XX	XX	ABB82231
XX	XX	XX	ID ABB82231 standard; protein; 687 AA.
XX	XX	XX	AC ABB82231;
XX	XX	XX	08-JAN-2003 (first entry)
XX	XX	XX	Human cPLA2/B splice variant (clone 19a).
XX	XX	XX	Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme; antiinflammatory; antiarthritic; antipsoziatic; antirheumatic; cytosolic; antiasthmatic; human.
XX	XX	XX	OS Homo sapiens.
XX	XX	XX	US2002106364-A1.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:05:39 ; Search time 88.6667 Seconds
(without alignments)
2996.666 Million cell updates/sec

Title: US-10-612-668-21

Perfect score: 3620

Sequence: 1 MQFFRLVNTFGVTNLFNS.....GAKELGKMVVDCCTPDGGRP 687

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3620	100.0	687	2 AAW17847	Aaw17847 Cytosolic
2	3620	100.0	687	5 ABB82231	Abb82231 Human cPL
3	3606.5	99.6	688	2 AAW17848	Aaw17848 Cytosolic
4	3606.5	99.6	688	5 ABB82232	Abb82232 Human cPL
5	3593.5	99.3	784	7 ADD93407	Add93407 Human lip
6	3566.5	98.5	806	5 AAE25968	Aae25968 Human PLA
7	3566.5	98.5	806	8 ADO19776	Ado19776 Human PRO
8	3544.5	97.9	810	8 ABM84355	Abm84355 Human dia
9	3544.5	97.9	810	8 ABM84354	Abm84354 Human dia
10	3302.5	91.2	752	2 AAR83018	Aar83018 Calcium-i
11	3302.5	91.2	752	2 AAW01479	Aaw01479 Calcium-i
12	3302.5	91.2	752	2 AAW13163	Aaw13163 Ca-indepe
13	3302.5	91.2	752	2 AAW17849	Aaw17849 Hamster c
14	3302.5	91.2	752	2 AAW81825	Aaw81825 Chinese h
15	3302.5	91.2	752	5 ABB82215	Abb82215 Calcium i
16	3257	90.0	751	7 ADD46244	Add46244 Rat Prote
17	3257	90.0	751	7 ADE60532	Ade60532 Rat Prote
18	3257	90.0	751	7 ADE55230	Ade55230 Rat Prote
19	3257	90.0	751	7 ADE60536	Ade60536 Rat Prote
20	2723	75.2	667	7 ADM05093	Adm05093 Human pro
21	2084	57.6	394	2 AAW17845	Aaw17845 Cytosolic
22	2084	57.6	394	5 ABB82229	Abb82229 Calcium i
23	1690.5	46.7	401	4 AAB32811	Aab92811 Human pro
24	1531	42.3	292	2 AAW17846	Aaw17846 Cytosolic
25	1531	42.3	292	5 ABB82230	Abb82230 Calcium i

ALIGNMENTS

RESULT 1

AAW17847

ID AAW17847 standard; protein; 687 AA.

XX AC AAW17847;

DT 07-AUG-1997 (first entry)

XX DE Cytosolic phospholipase A2/B (alternatively spliced clone 19a).

XX KW Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade; inflammation; inhibitor; antiinflammatory.

XX OS Homo sapiens.

XX PN WO9717448-A2.

XX PD 15-MAY-1997.

XX PF 07-NOV-1996; 96WO-US017794.

XX PR 08-NOV-1995; 95US-00555568.

XX (GEMY) GENETICS INST INC.

XX Jones S, Tang J;

XX WPI; 1997-281037/25.

XX DR N-PSDB; AAT68825.

XX PT Calcium independent phospholipase A2/B - used to reduce inflammation in a mammalian subject.

XX Claim 12; Page 49-51; 74pp; English.

XX A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17847) is characterised by activity in the absence of calcium, by activity in a mixed micelle assay with 1-palmitoyl-2-(14C)- arachidonyl-phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a lack of stimulation by ATP, and by including in its sequence at least one of the amino acid sequences given in AAW17839- 44). It is an alternatively spliced variant of another isolated polypeptide (AAW17845) and is encoded by an isolated cDNA (AAT68825). Other PLA2/B enzymes (AAW17846, AAW17848) have also been identified. sPLA2/B enzymes are thought to be involved in the release of arachidonic acid in specific tissues. Recombinant sPLA2/B polypeptides produced in transformed host cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory drugs which inhibit the arachidonic acid cascade

[illegible]

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Patizzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RL "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun. Release 3 of the *Drosophila*
 RT *melanogaster* euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003550; AAF50194.3; -;
 DR HSSP; O60778; 1OY3.
 DR FlyBase; FBgn0036053; CG6718.
 DR GO; GO:0003824; F.catalytic activity; IEA.
 DR GO; GO:0045733; F.nutrient reservoir activity; IEA.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; Ank; 4.
 DR Pfam; PF01734; Patatin.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00246; ANK; 6.

DR PROSITE; PSS0088; ANK_REPEAT; 3.
 DR PROSITE; PSS0297; ANK_REPEAT; 1.
 KW ANK repeat.
 SQ SEQUENCE 877 AA; 96862 MW; C9DC2CD6C282869B CRC64;
 Query Match 32.1%; Score 1163.5; DB 2; Length 877;
 Best Local Similarity 31.9%; Pred. No. 2e-79;
 Matches 257; Conservative 135; Mismatches 248; Indels 165; Gaps 12;
 QY 17 LFSNPFPRKVEAVADYTSDDRVREGQILFQNTNRTWDCVLNPNRSQSGFRFLQLEL 76
 DB 40 LFAPPF-----NSSNEKRAVVEILQRTSD-----SNTTSFSLYRSV 78
 QY 77 EADALVNHOYSSQLLPYESSQVILHTEVLOHLTLRNHPNSVAHLAVELGIRECPH 136
 DB 79 QOEAEERFNAFLQRLPVPVSVIKEYYNVGLQKACDALADNPSTLHLYAYFNLDVYIS 138
 QY 137 HSRISSCANCAENBGCPTPLHCLACKRGDEILVELVQYCHTQMDVTDYKGVTFVHAVQG 196
 DB 139 NPKMLQCVDDQADATLMSFPQLAIKQGHMEWVKALLPL--SKLEHLDINSNSVFHYAA-S 195
 QY 197 DNSQVLQLGRNAVAGLNQVANNQGLTPLHLACQLGKQEMVRVLLLCNARCNIMGNGYPI 256
 DB 196 TTKEITNLIIDKSTVNLNHLNSDGYTPLHVACLADKPNVVKALLAGANVNL--NAKDI 252
 QY 257 HSAMKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMARMLKRGNCVNSTSSA 316
 DB 253 RKVYKTSAPTTSVSPFLRTNVSKLYTQDMKYGGTPLHWCSSRETTHALIMEGCDVNATPD 312
 QY 317 GNTALHVGVMNRFPDCAVTLTHGANADARGHGTNPLHLAMSNDKVENMKALIVFGARV 376
 DB 313 GRTALHVVARNRFEVCVTLIAHDAIDVLDKGNALHIAIEKKLVPIVQCLVFGCDI 372
 QY 377 DTPNDFGETP-----TFLASKIG----- 394
 DB 373 NLKNKGKGTPRHVMGNDSAGNKNKDBILVILHSGVAKRCKDTGSKCPGCNAGNYGIPP 432
 QY 395 ----KLQDLMHISR-----ARKPAFI----- 411
 DB 433 EAPESVEQREHIEHMLATTSRQMMGGFLNAAANGILEKQQAOKPVVDTEKELKGQSIM 492
 QY 412 ----LGSMR-----DEKRTDHD 424
 DB 493 DALLGNFTTKVNADKEMKENSDDLSSASQKSAVSSPEQLPSPPTPIAAIEGDKPYGRGR 552
 QY 425 LCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGIILALAILHKSWMYMG 484
 DB 553 LCLDGGGIRGLVLVQMLEIEKLSRTPIIHMFWDIAGTSTGGIILALALCGCKTRQCMG 612
 QY 485 MYFRMKDEVFRGSRPYESGPLEEFKREFGEHTKTDVVKPKVMTLTGSLDRQPAELHLF 544
 DB 613 LYLRMKQCFVGSFRPNSEFFESILKDNLGEFNVMTDIKPKIMVTGVNADRPVDLHLF 672
 QY 545 RNYDAPETVR---EPRENQVNLRPAPPSDOLVRAARSAGAAATPYRPNRGRFLDGGLL 601
 DB 673 RNYTSASDILGIVTPINNRR---PPQPSQVLVRAARATGAATGAATGAFRFLDGGLI 729
 QY 602 ANNPITLDMTEIHEYNODLIRKQANKVKKLSIVVSLGTGRSPQVPTCVDFRPSNPWE 661
 DB 730 ANNPITLDMTEIHEYNMALSAGRESEALPVSVMVSLGTGHIPVTELKIDIDVFRPESWD 789
 QY 662 LAKTVFGAKELGKMWVDCTDPPDGR 686
 DB 790 TAKLAYGISTIGNLLVDQATCSDGR 814
 RESULT 11
 QYKUD4
 ID Q7KUD4
 AC Q7KUD4;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)

Db	600	YKSTATFQPLTVQGHEDDLVLGVYTRPPRKRVYTDDEQLVWRAARSSGAAPTFRPM	659
QY	593	GRFDGGLANNPTLDAMTEIHEYNOQLIRKQANKVKKLSIVVSLGTGRSPQVPTCV	652
Db	660	GRFDGGLANNPTLDAMTEIHFQNKALKAQGRDEVDTRLGVVSVLGTGKPPQVANSVD	719
QY	653	VFRPSNPWELAKTVFGAKELGKVMVDCCTDPDG	685
Db	720	VFRPSNPWELAKTVFGVVKELGKMLVDCCTDSG	752
RESULT 9			
ID	Q7Q2U1	PRELIMINARY; PRT; 879 AA.	
AC	Q7Q2U1;		
DT	01-MAR-2004 (TrEMBLrel. 26, Created)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	EbiP3359 (Fragment).		
GN	Names=ebiG3359; ORFNames=ENSANGG00000002698;		
OS	Anopheles gambiae str. PEST.		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.		
OX	NCBI_TaxID=180454;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=PEST;		
RA	Anopheles Genome Sequencing Consortium;		
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.		
CC	-!- CAUTION: The sequence shown here is derived from an		
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is		
CC	preliminary data.		
DR	EMBL; AAB01008968; EAA13225.1; -.		
DR	HSSP; P20749; 1K1B.		
DR	GO; GO:0003824; F: catalytic activity; IEA.		
DR	GO; GO:0045735; F: nutrient reservoir activity; IEA.		
DR	InterPro; IPR002110; ANK.		
DR	InterPro; IPR000560; HisAc phaptse.		
DR	InterPro; IPR002641; Patatin.		
DR	Pfam; PF00023; Ank; 6.		
DR	Pfam; PF01734; Patatin; 1.		
DR	PRINTS; PR01415; ANKYRIN.		
DR	PROSITE; PS50088; ANK REPEAT; 3.		
DR	PROSITE; PS50297; ANK REP REGION; 1.		
DR	PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.		
KW	ANK repeat.		
FT	NON_TER 1 1		
FT	NON_TER 879 879		
SQ	SEQUENCE 879 AA; 96484 MW; 3491E003CF637188 CRC64;		
Query Match			
Best Local Similarity 32.2%; Score 1164; DB 2; Length 879;			
Matches 260; Conservative 134; Mismatches 269; Indels 146; Gaps 9;			
QY	21	PRFVKEVAVADYTSRDRREGQLILFQNTPNR-----TWDCVLNPNRS--OSGRLQ 73	
Db	11	PNKVQEVKESYNLPIVQKNESMRLFAPNPNPKLVYVEILRPHSETINTSYSLR 70	
QY	74	LELEADALNVHFOYSSQLPFYESSQVQLHTEVLQHLTLIRNHPSPVAHLAVELGIRE 133	
Db	71	ATTQSAAEKFEAFHQRLPELVKIVREMYNINGLQKLDVLIDNPSWSLAHVAFYNLTD 130	
QY	134	CFHHSIIISCANCAENEGCTPLHLACRKGDEGLIVELYQYCHTQMDVTDYKGETVHYA 193	
Db	131	YISNPSIIDFLDYAEYSEMMTPLOQAVKANNIEFVKALIQSNQCNLEHLDKNSVHYA 190	
QY	194	VQGDNSQVLLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLLLCNARCNIMGPN 253	
Db	191	A-STTKEMINMLTAKTSNLNHCNTDGYTPLHLACLADKPCVKALLACADTNKYA-RG 248	
QY	254	YPIHSAMKTSQKCAEMITMSDSSQHSKDPYRGASPLHWAKNAEMRLKRGCVNST 313	
Db	249	AGTSYSKSISSNVADFLVS-NPNKLFPTQDMKHGGTPLHSSSSREVLSNIERGCDVNLV 307	

QY	314	SSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKALIVFG 373	
Db	308	NFNGQPTPLHVAVARDLECVVALLAHDAEIDVVDNSGNTPLHIAVEKCLPIVQCLVVF 367	
QY	374	AEVDTPNDPGEPTFL-----ASKGKLQDLMH----- 401	
Db	368	ADFNKENKDGKTPRHLVKGDDSGSKDMLIYLHVSAGKRCPEKSGKPCPGCAAGTYNG 427	
QY	402	-----ISRA 405	
Db	428	IPPAQPETTEQREHIQOVLARTTTKSHRNSVPSLISNTIRATIPERERPEVKTVDVSQE 487	
QY	406	RKPAFTILGSM-----RDEKRTHD----- 423	
Db	488	RKCAASMDALLSMFMSKVEAASKPTSPTSTSSSLKECAGSGGORTSRPRSSCEAGSGE 547	
QY	424	-----HLCLDGGGVKGLIIIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALILHSK 477	
Db	548	SYNGRGLLCLDGGGIRGLVLAQMLLEIENLAQTPIVHLFDWIAGTSTGGILALALCGCK 607	
QY	478	SNAYMGMYFRMKDEVFRGSRPYESGPLFEFLKREGEHTKMTDVRKPKVMLTGTLSDRQ 537	
Db	608	TKQKQCCLYLRMKDQAFVGSRPYPSPDQETVLKEQLGEFTVMSDIKHPRLMVTGVMDRK 667	
QY	538	PAELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDOLVWRAARSSGAAPTFRPNGRFLD 597	
Db	668	PVNLHLFRNYEASDILSVTSPNNRGQPPPPSEQLVWRAARATGAAPSYFRAFGRFLD 727	
QY	598	GGLLANNPTLDAMTEIHEYNOQLIRKQANKVKKLSIVVSLGTGRSPQVPTCVDFVRPS 657	
Db	728	GGLLANNPTLDAMTEIHELNAALHYIGRASEAVPVSVVSVSLGTGLTPVVDLKEIDVFRPD 787	
QY	658	NPWELAKTVFGAKELGKVMVDCCTDPGR 686	
Db	788	SIWATAKVAYGISTITLVLVDQATASDGR 816	
RESULT 10			
ID	Q9VT60	PRELIMINARY; PRT; 877 AA.	
AC	Q9VT60;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	CG6718-PA.		
GN	ORFNames=CG6718;		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;		
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,		
RA	Abril J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,		
RA	Balaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Botchan M.R., Boutch J., Brokstein P., Brotter P.,		
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,		
RA	Forster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,		
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,		

QY 121 SVHLAVELGIRECFHSHRIISCANCAENEBECTPLHLACRKGDEGIELVELVOYCHTQMD 180
 Db 121 SLAHVAEIGLSEKPHGILSLNSTECDCGSTPLHLACKCKGNCIQELVEECQARD 180
 QY 181 VTDYKGETVFHYAVQDINSQVQLLGRNAVAGLQVNNQGLTPLHLACOLGQKQEMVRVLL 240
 Db 181 IADQNGEIVYHAAQONPRVIEILCSVPSGVNKHNSNNETPLHVACELGKTELVLALL 240
 QY 241 LCNARCNIMGNGYPIHSAKFSQKGCAMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
 Db 241 RCHARCDIIGKDGYPITHAMKYSQCEVBAILDVSASQLHARDPRYQATPIHWAENA 300
 QY 301 RMLLRGCNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
 Db 301 RLIERGCNVNSTCTLDPLHIMWRDRFEAMVLLTNVADPNVKGEGHNTPLHLAMK 360
 QY 361 DNVEIMKALIVFGAEVDTFNDPFGETPTFLASKIGK-LQDLMIHSARK-----PAFILGSM 415
 Db 361 DQELIKALMWFGADVQEHNDGFGETPLGIAARSSKGFDPVVVSTALSGMLVPQDVTDFR 420
 QY 416 REKTRTHLLCLDGGGVKGLIIQLLIAEKASGVATKDLFDWVAGTSTGGILALAILH 475
 Db 421 EDGLRVKORLLCLDGGGIRGLVMQLLIAEKAAGRPIRELFDWVSGTSTGGILALAIH 480
 QY 476 SKSMAYMRGYFRMKDEVERGSRPYESGPLEFLKREFGHTKMTDVRKPKVMLTGTLS 535
 Db 481 GMPBSVRCLYFRMKNEVPHGRPYESGPLEFLKREFGHTKMTDVRKPKVMLTGTLS 540
 QY 536 ROPAEHLHFRNYDAPETVREPRFNQNVNLRPAQPSDQLVWRAARSSGAAPTYFRPNGRF 595
 Db 541 RHPAEHLHFRNYDPPETDHEPPYKSVASFRPVTTPAEQLVWRAARSSGAAPTYLRPMGRF 600
 QY 596 LDGGLANNPTLDAMTEIHEYNOGLIRKQANKVKLSIVSLGTRSPQVPTCVDFR 655
 Db 601 LDGGLSNNTLDAMTEIHEYNTCLKKGMAGQVKGLGIVSLGTGKPPQISVSGVDYFR 660
 QY 656 PSNPVELAKTVGAKELGKVVDCCTDPDG 685
 Db 661 PSNPVEWMTVVGARELGKVVDCCTDSG 690

RESULT 8
 QSNWY0
 ID Q6NRY0 PRELIMINARY; PRT; 818 AA.
 AC Q6NRY0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE ZGC:77476.
 GN ORFNames=ZGC:77476;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC067375; AAH67375.1; -;
 DR HSSP; P20749; 1K1B.
 DR ZFIN; ZDB-GENE-040426-2079; ZGC:77476.
 DR GO; GO:0003824; F: catalytic activity; IEA.
 DR GO; GO:0045735; F: nutrient reservoir activity; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002641; Patatin.
 DR Pfam; PF00023; Ank; 6.
 DR Pfam; PF01734; Patatin; 1.
 DR PRINTS; PRO1415; ANKYRIN.
 DR SMART; SM00248; ANK; 6.
 DR PROSITE; PS00088; ANK_REPEAT; 4.
 DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
 KW ANK repeat.
 SQ SEQUENCE 818 AA; 90691 MW; C7B5CD45401P8EA9 CRC64;
 Query Match 54.6%; Score 1977.5; DB 2; Length 818;
 Best Local Similarity 50.5%; Pred. No. 2.1e-141;
 Matches 380; Conservative 122; Mismatches 182; Indels 69; Gaps 4;
 QY 1 MQFFGRLVNTSGVNTLFSNPRVKEVAVADYTSDDRVEEQQLILFQNTNRTWDCVLV 60
 Db 1 MOFLGRILDTSSVSSLSFNPRVVDQLSDYNGKILHQOQGRALYRNQSQSDCLLL 60
 QY 61 NPNRSQSGFLFQLEADALVNFHQSQQLPFYESSQVLTHTVQLHLTLIRNHPSW 120
 Db 61 CPESPSVALRMFQVASEEDAMNWFQYALKLRFYEMLRPPLKPEMLQPIVDCVRNHPDM 120
 QY 121 SVHLAVELGIRECFHSHRIISCANCAENEBECTPLHLACRKGDEGIELVELVOYCHTQMD 180
 Db 121 SSAHIAVDTGLRDLCKHNVILSQMN-SRDAQQTPLHLACERGDVGCVRLEECQARTD 179
 QY 181 VTDYKGETVFHYAVQDINSQVQLLGRNAVAGLQVNNQGLTPLHLACOLGQKQEMVRVLL 240
 Db 180 VKDKNGETPMHCAAKQDSALIIIEVLCAQAGVNSLNAAGETPMHIAICRLGVEVVKGLL 239
 QY 241 LCNARCNIMGNGYPIHSAKFSQKGCAMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
 Db 240 AGGARCDIMGNGFFIHTAMKFSKCAEILUSSPNQLLAEDPVYGGTPLHWAKTAMS 299
 QY 301 RMLLRGCNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
 Db 300 RLILDRGCNVNYSKTESPLHLTKRGRFEAAWTLTHGADANIRGQDNTALHLAMKL 359
 QY 361 DNVEIMKALIVFGAEVDTFNDPFGETPTFLASKIGK----- 395
 Db 360 DNMDLIKALMWFGADVVEHNDVGETPGLTAARTSKGNSNRKVLNMLCSVGVRECHPPPSLN 419
 QY 396 -----LQDLMIHS-----RARKPAFILGSMRDEKRTDHLCLDGGGVKGLI 437
 Db 420 SPTHSLRKAPPGICGFDIMQVAVATMSRGFVEADGLKTCNKMDRLCLDGGGKGLV 479
 QY 438 IQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHSAKSMAYMRGYFRMKDEVFRGS 497
 Db 480 LIQLLIAIEKAGRPIRELFDWVSGTSTGGILALAILHSAKSMAYMRGYFRMKDEVFRGS 539
 QY 498 RYESGPLEEFLKREFGHTKMTDVRKPKVMLTGTLSROPAEHLHFRNYDAPETVREPR 557
 Db 540 RYESGPLEEFLKREFGHTKMTDVRKPKVMLTGTLSROPAEHLHFRNYDAPETVREPR 599
 QY 558 FNQNVNLRPPAOP-----SDQLVWRAARSSGAAPTYFRN 592

DR	PRINTS; PRO1415; ANKYRIN.	DT	25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DR	SMART; SM00248; ANK; 6.	DT	25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DR	PROSITE; P850088; ANK REPEAT; 4.	DE	MGC83523 protein.
DR	PROSITE; P850297; ANK_REP_REGION; 1.	GN	Name=MGC83523;
KW	ANK repeat; Hydrolase; Lipid degradation; Repeat.	OS	Xenopus laevis (African clawed frog).
FT	REPEAT 150 180 ANK 1.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
FT	REPEAT 184 214 ANK 2.	OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
FT	REPEAT 218 247 ANK 3.	OC	Xenopodinae; Xenopus.
FT	REPEAT 250 280 ANK 4.	OX	NCBI_TaxID=8355;
FT	REPEAT 285 311 ANK 5.	RN	[1]_TaxID=8355;
FT	REPEAT 315 344 ANK 6.	RP	SEQUENCE FROM N.A.
FT	REPEAT 348 377 ANK 7.	RC	TISSUE=Eye;
FT	ACT SITE 464 464 Potential.	RX	MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
SQ	SEQUENCE 751 AA; 83582 MW; 393BBADA7FCC99B CRC64;	RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Query Match		RA	Richardson P.;
Best Local Similarity 89.7%; Score 3257; DB 1; Length 751;		RT	"Genetic and genomic tools for Xenopus research: The NIH Xenopus
Matches 616; Conservative 29; Mismatches 40; Indels 2; Gaps 2;		RL	Dev. Dyn. 225:384-391(2002).
		RN	[2]
QY	1 MOFFGRLVNTFSGVTLNFSNPRFVKEVAVADYTSDDRVREEGQILFQNTPNRTWDCVLV 60	RP	SEQUENCE FROM N.A.
Db	1 MOFFGRLVNTLSSVTLNFSNPFRAKEVSLADYASSERVREEGQILQLQNASRNTWDCVLV 60	RC	TISSUE=Eye;
QY	61 NPNRSQSGRLPQLELEADALVNFOYSSQLPFFYESSQVLHTEVLQHLTDLIRNHPSW 120	RA	Strausberg R.L., Feirngold E.A., Grouse L.H., Derge J.G.,
Db	61 SPNPNQSDRLFOLESEADVLNFOYSSQLPFFYESSQVLHVEVLQ-LTDLIRNHPSW 119	RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
QY	121 SVAHLAVALGIRECFHSHRIISCANCAENEECTPLHLACRGDGEILVELVQYCHTQMD 180	RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Db	120 TVTHLAVALGIRECFHSHRIITCANSTENBEGCTPLHLACRGDSILVELVQYCHAQMD 179	RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
QY	181 VTDYKGETVFHVAVQGDNSQVLQIGRNAVAGLNQVNNQGLTPLHLACOLGQEMVRVLL 240	RA	Diatchenko L., Marudani K., Farmer A.A., Rubin G.M., Hong L.,
Db	180 VTDNKGETAHVAVQGDNPQVLQIGNASAGLNQVNNQGLTPLHLACOMGQEMVRVLL 239	RA	Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
QY	241 LCNARNCINMGPGYPIHSAKMSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300	RA	Brownstein M., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Db	240 LCNARNCINMGPGFPIHTAKMSQKCAEMIISMDSNQIHSKDPYRGASPLHWAKNAEMA 299	RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
QY	301 RMLLRKGCNVNSTSAGNTALHVGWRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360	RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Db	300 RMLLRKGCVDVSTASGNTALHVAVTRNRFDCVMVLLTTYGANAGARGEHNTPLHLAMSK 359	RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
QY	361 DNVEIMKALIVGAEDVTDNDGETTETLASKIGK-LQDLMHISRARKPAFTLGSMDK 419	RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Db	360 DNVEWKALIVGAEDVTDNDGETTETPAISKISKQLQDLMPVSRARKPAFTLSSMDK 419	RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
QY	420 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSQM 479	RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Db	420 RTHDHLCLDGGVGKGLVIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSQM 479	RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
QY	480 AYMRGMYFRMKDEVFRGSRPYSGPLBEFLKREFGHEHTKMTDVRKPKVMTLGTLSRQPA 539	RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Db	480 AYMRGYFRMKDEVFRGSRPYSGPLBEFLKREFGHEHTKMTDVKPKVMTLGTLSRQPA 539	RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
QY	540 ELHLFNNYDAPETVREPRNQNVNLRPPAQPDSOLVRAARSGGAAPTFRNGRLDGG 599	RA	Jones S.J., Marra M.A.;
Db	540 ELHLFNNYDAPAVREPTCPNINLKPPTQPADQLVRAARSGGAAPTFRNGRLDGG 599	RT	"Generation and initial analysis of more than 15,000 full-length human
QY	600 LLANNPTLDAMTEIHEYNQDLIRKQANKYKKLISIVVSLGTGRSPQVPVTCVDVFRPSNP 659	RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
Db	600 LLANNPTLDAMTEIHEYNQDMIRKQGNKVKKLISIVVSLGTGKSPQVPVTCVDVFRPSNP 659	RN	[3]
QY	660 WELAKTVFGAKELGKMWVDCCTDPDR 686	RP	SEQUENCE FROM N.A.
Db	660 WELAKTVFGAKELGKMWVDCCTDPDR 686	RC	TISSUE=Eye;
RESULT 7		RA	Klein S., Gerhard D.S.;
ID	Q6DDKO PRELIMINARY; PRT; 756 AA.	RL	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
AC	Q6DDKO;	DR	EMBL; BC077558; AAH77558.1; -.
DT	25-OCT-2004 (TReMBLrel. 28, Created)	DR	GO; GO:0003824; P.catalytic activity; IEA.
		DR	GO; GO:0045735; P.nutrient reservoir activity; IEA.
		DR	InterPro; IPR002110; ANK.
		DR	InterPro; IPR002641; Patatin.
		DR	Pfam; PF00023; ANK; 7.
		DR	Pfam; PF01734; Patatin; 1.
		DR	PRINTS; PR01415; ANKYRIN.
		DR	SMART; SM00248; ANK; 7.
		DR	PROSITE; PS50088; ANK_REPEAT; 3.
		KW	ANK repeat.
		SQ	SEQUENCE 756 AA; 84303 MW; C0278741CCAS2A71 CRC64;
		Query Match	
		Best Local Similarity 61.1%; Score 2210.5; DB 2; Length 756;	
		Matches 413; Conservative 120; Mismatches 152; Indels 5; Gaps 2;	
QY	1 MOFFGRLVNTFSGVTLNFSNPRFVKEVAVADYTSDDRVREEGQILFQNTPNRTWDCVLV 60	QY	1 MOFFGRLVNTFSGVTLNFSNPRFVKEVAVADYTSDDRVREEGQILFQNTPNRTWDCVLV 60
Db	1 MDLFGRIFTVTSVAVTNLFSNPKYREVPLSEYSGSSCLQEDGEMLLYRNRTAKSLDCVLV 60	Db	1 MDLFGRIFTVTSVAVTNLFSNPKYREVPLSEYSGSSCLQEDGEMLLYRNRTAKSLDCVLV 60
QY	61 NPNRSQSGRLPQLELEADALVNFOYSSQLPFFYESSQVLHTEVLQHLTDLIRNHPSW 120	QY	61 NPNRSQSGRLPQLELEADALVNFOYSSQLPFFYESSQVLHTEVLQHLTDLIRNHPSW 120
Db	61 NPSSPQNAVRLPQLESEPEALCRFOYAVKLPFRFVSSRKGCLCLETQQLTDCIRHPNW 120	Db	61 NPSSPQNAVRLPQLESEPEALCRFOYAVKLPFRFVSSRKGCLCLETQQLTDCIRHPNW 120

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RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RX PubMed:12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore I., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC081916; AAH81916.1; -
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR PRINTS; PR01734; Patatin; 1.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Hypothetical protein.
SQ SEQUENCE 807 AA; 89555 MW; 1B9018AE1B2D252F CRC64;

Query Match
Best Local Similarity 90.3%; Score 3268; DB 2; Length 807;
Matches 621; Conservative 29; Mismatches 36; Indels 56; Gaps 1;

QY 1 MQFFGRLVNTFGVTLNFSNPRFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVILV 60
DB 1 MQFFGRLVNTLSSVTLNFSNPRFRVKEVSLADYASSERVREEGQLILQNASRNTWDCVILV 60
QY 61 NPNRSQSGRLFOLEADALVNFHOYSQQLPPFYESSQVVLHTEVLQHLTDLIRNHPSW 120
DB 61 SPRNPSQSGRLFOLEADALVNFHOYSQQLPPFYESSQVVLHTEVLQHLTDLIRNHPSW 120
QY 121 SVAHLAVALGIRECFHSHRIISCANCAENEECTPLHLACRGDGEILVELVQYCHTQMD 180
DB 121 TVTHLAVALGIRECFHSHRIISCANSTENEGCTPLHLACRGDSEILVELVQYCHAQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNVNQLGTPHLHLACQLGQKQEMVRVLL 240
DB 181 VTDNKGETAHYAVQGDNPQVLQLGKNASAGLNVNQLGTPHLHLACQMGQEMVRVLL 240
QY 241 LCNARCNMGNGPYTHSANKFSQKCAEMIISMOSQTHSDKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNMGPGFPHTHTAMKFSQKCAEMIISMDSNQTHSDKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRGCNVNSTSSAGNTALHGVNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRGCNVDSASGNTALHGVNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVMEMIKALIVGAEDVTDNDFGCTPTFLASKIGK----- 395
DB 361 DNMEWVALIVGAEDVTDNDFGCTPTFLASKISKILTRKALLTLTKVTGADYHFFPIQG 420
QY 396 -----LQDLMHISRRKPAFPLGSMRDEKRTDHDH 424

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RESULT 6

PA26 RAT

ID PA26 RAT

AC 97570;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (CaI-

DE PLA2) (Group VI phospholipase A2) (GVI PLA2).

GN Name=Pla2g6;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Pancreatic islets;

RX MEDLINE=97269008; PubMed=9111008; DOI=10.1074/jbc.272.17.11250;

RA Ma Z., Ramanadham S., Kempe K., Chi X.S., Ledenson J., Turk J.;

RT "Pancreatic islets express a Ca2+-independent phospholipase A2 enzyme

RT that contains a repeated structural homologous to the integral

RT membrane protein binding domain of ankyrin.";

RL J. Biol. Chem. 272:11118-11127(1997).

CC -!- FUNCTION: Catalyzes the release of fatty acids from phospholipids.

CC It has been implicated in normal phospholipid remodeling, nitric

CC oxide-induced or vasopressin-induced arachidonic acid release and

CC in leukotriene and prostaglandin production. May participate in

CC fas mediated apoptosis and in regulating transmembrane ion flux in

CC glucose-stimulated B-cells.

CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-

CC acylglycerophosphocholine + a carboxylate.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- TISSUE SPECIFICITY: Found in brain, lung, spleen, kidney, liver,

CC heart and skeletal muscle.

CC -!- SIMILARITY: Contains 7 ANK repeats.

CC

CC

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CC

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QY 540 ELHLFRNYDAPETVTRPRFNQNVNLRPPAQPSDOLVWRAARSSGAAPTYPFRPNGRFLDGG 599
Db 541 ELHLFRNYDAPEAVREPRCNQNLNKPPTQPADQLVWRAARSSGAAPTYPFRPNGRFLDGG 600
QY 600 LLANNPTLDAMTEIHEYNODLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNP 659
Db 601 LLANNPTLDAMTEIHEYNODMIRKQGNKVKLSIVVSLGTGKSPQVPTCVDFRPSNP 660
QY 660 WELAKTVFGAKELGKMVVDCTDPDGR 686
Db 661 WELAKTVFGAKELGKMVVDCTDPDGR 687

RESULT 4
Q9JK61
ID Q9JK61 PRELIMINARY; PRT; 807 AA.
AC Q9JK61
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ca2+-independent phospholipase A2 long form (Pla2g6 protein).
GN Name:Pla2g6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIH/Swiss;
RA Chiu C.-H., Jackowski S.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF259401; AAF72651.1; -.
DR EMBL; BC057209; AAH57209.1; -.
DR HSSP; Q60778; 10Y3
DR MGD; MGI:1859152; Pla2g6.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR PRINTS; PR01734; Patatin; 1.
DR PROSITE; PS0088; ANK_REPEAT; 4.
DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
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KW ANK repeat.
SQ SEQUENCE 807 AA; 89559 MW; 3838889731100294 CRC64;

Query Match
Best Local Similarity 90.4%; Score 3272; DB 2; Length 807;
Matches 622; Conservative 29; Mismatches 35; Indels 56; Gaps 1;

QY 1 MQFFGRLVNTFSGVTNLFNSNPRFRVKEVAVADYTSRVRREBEGQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGRLVNTLSSVTNLFNSNPRFRVKEVSLTDYVSSRVEREAGQLILLQVNSRNTWDCVLV 60
QY 61 NPNRSQSGRLFLQLELEADALVNFHOYSQQLLPFFYESSQVLHTEVLOHLTDLIRNHPWS 120
Db 61 SPNRSQSGRLFLQLESEADALVNFQFSSQLPPFYESSQVLHVEVLOHLTDLIRNHPWS 120
QY 121 SYAHLVAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDSILVELVOYCHTOMD 180
Db 121 TVTHLAVELGIRECFHHSRIISCANSTENEECTPLHLACRKGDSILVELVOYCHTOMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDNKGETAHYAVQGDNFQVLQLGKNASAGLNQVNNQGLTPLHLACRKGQEMVRVLL 240
QY 241 LCNARCNIIMPNGYPIHSAKFQSKGCAEMIISMDSSQIHSKDPYRGASPLHWKNAEMA 300
Db 241 LCNARCNIIMPNGGPIHTAMKFSQKGAEMIISMDSNQIHSKDPYRGASPLHWKNAEMA 300
QY 301 RMLLKRCGNVNTSSAGNTALHVGVRNRPDCAIIVLLTHGANADARGEHGTPLHLAMSK 360
Db 301 RMLLKRCGVDSTSSGNTALHVAVMNRNFDVCMVLLTYGANAGARGEHGTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIGK----- 395
Db 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIGK----- 395
QY 396 -----LQDLMHISRARKPAFILGSMRDEKERTHDH 424
Db 421 VSTEQSSAAATHPLFSLDRTQPAISLNLLEQLDLMPISRARKPAFILGSMRDEKERTHDH 480
QY 425 LILCLDGGVKGILLIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHSKSMAYMRG 484
Db 481 LLCLDGGVKGILLIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHSKSMAYMRG 540
QY 485 MYFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPAELHLF 544
Db 541 VYFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPAELHLF 600
QY 545 RNYDAPETVREPRFNQNVNLRPPAQPSDOLVWRAARSSGAAPTYPFRPNGRFLDGLANN 604
Db 601 RNYDAPEAVREPRCNQNLNKPPTQPADQLVWRAARSSGAAPTYPFRPNGRFLDGLANN 660
QY 605 PILDAMTEIHEYNODLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNPHELAK 664
Db 661 PILDAMTEIHEYNODMIRKQGNKVKLSIVVSLGTGKSPQVPTCVDFRPSNPHELAK 720
QY 665 TVFGAKELGKMVVDCTDPDGR 686
Db 721 TVFGAKELGKMVVDCTDPDGR 742

RESULT 5
Q66HD1
ID Q66HD1 PRELIMINARY; PRT; 807 AA.
AC Q66HD1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
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QY 1 MOFFGRLVNTSGVNTLFSNPRFVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
D 1 MOFFGRLVNTSSVNTLFSNPRFVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGRLFOLEADALVNFHOYSQQLPFYESSQVLTHTVLOHLDLIRNHP 120
D 61 SPNPSQSGRLFOLEADALVNFHOYSQQLPFYESSQVLTHTVLOHLDLIRNHP 120
QY 121 SYAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEIIVLVQYCHTQMD 180
D 121 TVTHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEIIVLVQYCHTQMD 180
QY 181 VTDYKGETVHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGQEMVRVLL 240
D 181 VTDNKGETAFAHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGQEMVRVLL 240
QY 241 LCNARCNIMGNGYPIHTAMKFSQKCAEMIISDSSQIHSKDPYRGASPLHWAKNAEWA 300
D 241 LCNARCNIMGNGYPIHTAMKFSQKCAEMIISDSSQIHSKDPYRGASPLHWAKNAEWA 300
QY 301 RMLKRGCVNSTSGAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
D 301 RMLKRGCVNSTSGAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVMEMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMHISRARKPAFPLGSMRDEK 419
D 361 DNVMEMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMHISRARKPAFPLGSMRDEK 419
QY 420 RTHDHLCLDGGVKGVLIIQLLIIAEKASGATKDLFDWVAGTSGGILALAILHKS 479
D 420 RTHDHLCLDGGVKGVLIIQLLIIAEKASGATKDLFDWVAGTSGGILALAILHKS 479
QY 480 AYMRGMYFMKDEVRGSRPYSGPLEEFKKEFGEHTKMTDVRKPKVMTGTLSDRQPA 539
D 480 AYMRGMYFMKDEVRGSRPYSGPLEEFKKEFGEHTKMTDVRKPKVMTGTLSDRQPA 539
QY 600 LLANNPTLDAMTEIHEYNDLRKQKANKVKSLSIVSLGTCRSQVPTVCVDVFRPSNP 659
D 600 LLANNPTLDAMTEIHEYNDLRKQKANKVKSLSIVSLGTCRSQVPTVCVDVFRPSNP 659
QY 660 WELAKTVFGAKELGKXVDCCTDPDGR 686
D 660 WELAKTVFGAKELGKXVDCCTDPDGR 687

RESULT 3
Q7TPX2 PRELIMINARY; PRT; 752 AA.
AC Q7TPX2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phospholipase A2, group VI.
GN Name=Pla2g6;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus..
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He; TISSUE=Osteoblast;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He; TISSUE=Osteoblast;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052845; AAHS2845.1; -.
DR HSSP; P07207; 1078.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002841; Pacatin.
DR Pfam; PF00023; ANK; 6.
DR Pfam; PF01734; Pacatin; 1.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS00297; ANK_REPEAT_REGION; 1.
KW ANK repeat. 752 AA; 83717 MW; DAC3347B0E14A AFC CRC64;
SQ
Query Match 90.9%; Score 3289.5; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 2, 9e-241;
Matches 621; Conservative 29; Mismatches 36; Indels 1; Gaps 1;
QY 1 MOFFGRLVNTSGVNTLFSNPRFVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
D 1 MOFFGRLVNTSSVNTLFSNPRFVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGRLFOLEADALVNFHOYSQQLPFYESSQVLTHTVLOHLDLIRNHP 120
D 61 SPNPSQSGRLFOLEADALVNFHOYSQQLPFYESSQVLTHTVLOHLDLIRNHP 120
QY 121 SYAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEIIVLVQYCHTQMD 180
D 121 TVTHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEIIVLVQYCHTQMD 180
QY 181 VTDYKGETVHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGQEMVRVLL 240
D 181 VTDNKGETAFAHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGQEMVRVLL 240
QY 241 LCNARCNIMGNGYPIHTAMKFSQKCAEMIISDSSQIHSKDPYRGASPLHWAKNAEWA 300
D 241 LCNARCNIMGNGYPIHTAMKFSQKCAEMIISDSSQIHSKDPYRGASPLHWAKNAEWA 300
QY 301 RMLKRGCVNSTSGAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
D 301 RMLKRGCVNSTSGAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVMEMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMHISRARKPAFPLGSMRDEK 419
D 361 DNVMEMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMHISRARKPAFPLGSMRDEK 419
QY 420 RTHDHLCLDGGVKGVLIIQLLIIAEKASGATKDLFDWVAGTSGGILALAILHKS 479
D 420 RTHDHLCLDGGVKGVLIIQLLIIAEKASGATKDLFDWVAGTSGGILALAILHKS 479
D 421 RSHDHLCLDGGVKGVLIIQLLIIAEKASGATKDLFDWVAGTSGGILALAILHKS 480
QY 480 AYMRGMYFMKDEVRGSRPYSGPLEEFKKEFGEHTKMTDVRKPKVMTGTLSDRQPA 539
D 480 AYMRGMYFMKDEVRGSRPYSGPLEEFKKEFGEHTKMTDVRKPKVMTGTLSDRQPA 539
D 481 AYMRGMYFMKDEVRGSRPYSGPLEEFKKEFGEHTKMTDVRKPKVMTGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPQNQNLKPPQADQLVWRAARSGAAPTFRPNRGLDGG 599
D 540 ELHLFRNYDAPETVREPQNQNLKPPQADQLVWRAARSGAAPTFRPNRGLDGG 599
QY 600 LLANNPTLDAMTEIHEYNDLRKQKANKVKSLSIVSLGTCRSQVPTVCVDVFRPSNP 659
D 600 LLANNPTLDAMTEIHEYNDLRKQKANKVKSLSIVSLGTCRSQVPTVCVDVFRPSNP 659
QY 660 WELAKTVFGAKELGKXVDCCTDPDGR 686
D 660 WELAKTVFGAKELGKXVDCCTDPDGR 687
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[6]
SEQUENCE FROM N.A.
RA MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
RX Dunham I., Hunt L.R., Collins J.E., Bruskewich R., Beare D.M.,
RA Clump M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Coward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd O.T.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann M.T.,
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull L., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA Fullon R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Letraile P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
RA Wilson R., Bedell J.A., Haller L.W., Mardis E., Waterston R.,
RA Korfiot I., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Peyrard M., Kedra D., Serousi E., Fransson I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenreich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
[7]
SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Catalyzes the release of fatty acids from phospholipids.
CC It has been implicated in normal phospholipid remodeling, nitric
CC oxide-induced or vasopressin-induced arachidonic acid release and

in leukotriene and prostaglandin production. May participate in
fas mediated apoptosis and in regulating transmembrane ion flux in
glucose-stimulated B-cells.
-!- FUNCTION: Isoform ankyrin-iPLA2-1 and isoform ankyrin-iPLA2-2,
which lack the catalytic domain, are probably involved in the
negative regulation of iPLA2 activity.
-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
acylglycerophosphocholine + a carboxylate.
-!- SUBUNIT: Forms large oligomeric 270-350 kDa structures.
-!- SUBCELLULAR LOCATION: Isoform LH-IPLA2 was found to be membrane
bound. Isoform SH-IPLA2 is cytoplasmic.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
Name=LH-IPLA2;
IsoId=O60733-1; Sequence=Displayed;
Name=SH-IPLA2;
IsoId=O60733-2; Sequence=VSP_000278;
Name=Ankyrin-iPLA2-1;
IsoId=O60733-3; Sequence=VSP_000281, VSP_000282;
Name=Ankyrin-iPLA2-2;
IsoId=O60733-4; Sequence=VSP_000277, VSP_000279, VSP_000280;
-!- TISSUE SPECIFICITY: Four different transcripts were found to be
expressed in a distinct tissue distribution.
-!- SIMILARITY: Contains 7 ANK repeats.

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or send an email to license@isb-sib.ch.

EMBL; AF064594; AAC97486.1; -
EMBL; AF102988; AAD41722.1; -
EMBL; AF102989; AAD41723.1; -
EMBL; AF117692; AAD30424.1; -
EMBL; AF117677; AAD30424.1; JOINED.
EMBL; AF117678; AAD30424.1; JOINED.
EMBL; AF117679; AAD30424.1; JOINED.
EMBL; AF117680; AAD30424.1; JOINED.
EMBL; AF117681; AAD30424.1; JOINED.
EMBL; AF117682; AAD30424.1; JOINED.
EMBL; AF117683; AAD30424.1; JOINED.
EMBL; AF117684; AAD30424.1; JOINED.
EMBL; AF117685; AAD30424.1; JOINED.
EMBL; AF117686; AAD30424.1; JOINED.
EMBL; AF117687; AAD30424.1; JOINED.
EMBL; AF117688; AAD30424.1; JOINED.
EMBL; AF117689; AAD30424.1; JOINED.
EMBL; AF117690; AAD30424.1; JOINED.
EMBL; AF117691; AAD30424.1; JOINED.
EMBL; AF116267; AAF34728.1; -
EMBL; AF116252; AAF34728.1; JOINED.
EMBL; AF116253; AAF34728.1; JOINED.
EMBL; AF116254; AAF34728.1; JOINED.
EMBL; AF116255; AAF34728.1; JOINED.
EMBL; AF116256; AAF34728.1; JOINED.
EMBL; AF116257; AAF34728.1; JOINED.
EMBL; AF116258; AAF34728.1; JOINED.
EMBL; AF116259; AAF34728.1; JOINED.
EMBL; AF116260; AAF34728.1; JOINED.
EMBL; AF116261; AAF34728.1; JOINED.
EMBL; AF116262; AAF34728.1; JOINED.
EMBL; AF116263; AAF34728.1; JOINED.
EMBL; AF116264; AAF34728.1; JOINED.
EMBL; AF116265; AAF34728.1; JOINED.
EMBL; AF116266; AAF34728.1; JOINED.
EMBL; AL080187; CAB45768.1; ALT_INIT.
EMBL; AY522921; CAB92478.1; -
EMBL; AL022322; CAA18446.1; -
EMBL; BC036742; AAB36742.2; -
EMBL; BC051904; AAB51904.1; -

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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:06:44 ; Search time 111.667 Seconds
(without alignments)
3150.433 Million cell updates/sec

Title: US-10-612-668-21

Perfect score: 3620

Sequence: 1 MQFFGLVNTFGVTNLFN.....GAKELGKVMVDCCTDPDGRP 687

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3566.5	98.5	806	1 PA26 HUMAN	O60733 homo sapien
2	3299.5	91.1	752	1 PA26 MOUSE	P97819 mus musculus
3	3289.5	90.9	752	2 Q7TPE2	O778X2 mus musculus
4	3272	90.4	807	2 Q9JK61	Q9JK61 mus musculus
5	3268	90.3	807	2 Q66HD1	Q66HD1 rattus norv
6	3257	90.0	751	1 PA26 RAT	P97570 rattus norv
7	2210.5	61.1	756	2 Q6DDK0	Q6DDK0 xenopus lae
8	1977.5	54.6	818	2 Q6NNY0	Q6NNY0 brachydanio
9	1164	32.2	879	2 Q7Q2U1	Q7Q2U1 anopheles g
10	1163.5	32.1	877	2 Q9VT60	Q9VT60 drosophila
11	1163.5	32.1	887	2 Q7KUD4	Q7KUD4 drosophila
12	742	20.5	386	2 Q8MR13	Q8MR13 drosophila
13	647.5	17.9	1071	2 Q20500	Q20500 caenorhabdi
14	634.5	17.5	1023	2 Q62398	Q62398 caenorhabdi
15	629.5	17.4	1021	2 Q81006	Q81006 caenorhabdi
16	458	12.7	762	2 Q95YD2	Q95YD2 caenorhabdi
17	357.5	9.9	501	2 Q9NSL3	Q9NSL3 caenorhabdi
18	338	9.3	843	2 P97582	P97582 rattus norv
19	338	9.3	1219	2 Q8C8R3	Q8C8R3 mus musculus
20	332	9.2	1863	2 Q723L5	Q723L5 homo sapien
21	332	9.2	3924	1 ANK22 HUMAN	Q01484 homo sapien
22	324.5	9.0	1004	2 Q7JNZ0	Q7JNZ0 caenorhabdi
23	324.5	9.0	1786	2 Q17344	Q17344 caenorhabdi
24	324.5	9.0	1809	2 Q17487	Q17487 caenorhabdi
25	324.5	9.0	1815	2 Q17488	Q17488 caenorhabdi
26	324.5	9.0	1841	2 Q8MGX0	Q8MGX0 caenorhabdi
27	324.5	9.0	1867	2 Q17486	Q17486 caenorhabdi
28	324.5	9.0	2039	2 Q17489	Q17489 caenorhabdi
29	324.5	9.0	6994	2 Q17343	Q17343 caenorhabdi
30	324.5	9.0	6994	2 Q17490	Q17490 caenorhabdi
31	320	8.8	1549	2 Q24241	Q24241 drosophila

ALIGNMENTS

RESULT 1

ID	PA26 HUMAN	STANDARD:	PRT:	806 AA.
AC	O60733; O75645; Q8N452; Q9UG29; Q9UIT0; Q9Y671;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (Cal-PLA2) (Group VI phospholipase A2) (GVI PLA2).			
GN	Name=PLA2G6; Synonyms=IPLA2;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2; ANKYRIN-IPLA2-1 AND ANKYRIN-IPLA2-2).			
RC	TISSUE=B-cell, and Testis;			
RX	MEDLINE=98079046; PubMed=9417066; DOI=10.1074/jbc.273.1.207;			
RA	Larsson P.K.A., Claesson H.-E., Kennedy B.P.;			
RT	"Multiple splice variants of the human calcium-independent phospholipase A2 and their effect on enzyme activity.";			
RL	J. Biol. Chem. 273:207-214(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2).			
RC	TISSUE=Pancratic islets;			
RX	MEDLINE=99194813; PubMed=10092647; DOI=10.1074/jbc.274.14.9607;			
RA	Ma Z., Wang X., Nowatzke W., Ramanadham S., Turk J.;			
RT	"Human pancreatic islets express mRNA species encoding two distinct catalytically active isoforms of group VI phospholipase A2 (iPLA2) that arise from an exon-skipping mechanism of alternative splicing of the transcript from the iPLA2 gene on chromosome 22q13.1.";			
RL	J. Biol. Chem. 274:9607-9616(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.			
RX	MEDLINE=9926033; PubMed=10336645;			
RA	Larsson Forsell P.K.A., Kennedy B.P., Claesson H.-E.;			
RT	"The human calcium-independent phospholipase A2 gene. Multiple enzymes with distinct properties from a single gene.";			
RL	Eur. J. Biochem. 262:575-585(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM LH-IPLA).			
RC	TISSUE=Testis;			
RA	Ansoerge W., Winkler U., Mewes H.-W., Gassenhuber J., Wiemann S.;			
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A., AND VARIANTS ILE-58; GLY-63; GLN-70; ASN-183 AND THR-343.			
RA	Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,			
RA	Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,			
RA	Sherwood J.K., Sherwood A.M., Leithauer B.J., Nickerson D.A.;			
RT	"NIHES-SNPs, environmental genome project, NIHES ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";			
RT	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.			

Q9V4B1 drosophila
Q8JHU3 brachydanio
Q7QKD3 anopheles g
Q8SWY2 drosophila
Q9NCP8 drosophila
Q7KU92 drosophila
Q9TYE0 caenorhabdi
Q9ERK0 mus musculus
Q9N180 bos taurus
Q88521 rattus norv
Q7Q196 brachydanio
Q70511 rattus norv
Q8VC68 mus musculus

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A>Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane
A:Reference number: PC2220; MUID:95071348; PMID:7526850
A:Accession: PC2220
A:Molecule type: protein
A:Residues: 910-929 <HER>
R:Davis, L.H.; Bennett, V.
J. Biol. Chem. 265, 10589-10596, 1990
A>Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger
A:Reference number: A35443; MUID:90285190; PMID:2141335
A:Accession: A35443
A:Molecule type: protein
A:Residues: 'X', '5', 'X', '7', '12', '403-417', 'X', '419-422', 'H', '424', 'LQ', '797-800', 'L', '802-814', '862-863',
C:Genetics:
A:Gene: GDB:ANK1; ANK
A:Cross-references: GDB:118737; OMIM:182900
A:Map position: 8p11.2-8p11.2
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing; phosphoprotein
F:2-1881/Product: ankyrin 1, erythrocyte form 1 #status predicted <MAT1>
F:2-1512,1675-1881/Product: ankyrin 2.2, erythrocyte #status predicted <MAT2>
F:2-827/Domain: 89K #status predicted <DOM1>
F:2-827/Region: anion exchange protein binding
F:44-76/Domain: ankyrin repeat homology <AN01>
F:77-109/Domain: ankyrin repeat homology <AN02>
F:110-142/Domain: ankyrin repeat homology <AN03>
F:143-171/Domain: ankyrin repeat homology <AN04>
F:172-204/Domain: ankyrin repeat homology <AN05>
F:205-237/Domain: ankyrin repeat homology <AN06>
F:238-270/Domain: ankyrin repeat homology <AN07>
F:271-303/Domain: ankyrin repeat homology <AN08>
F:304-336/Domain: ankyrin repeat homology <AN09>
F:337-369/Domain: ankyrin repeat homology <AN10>
F:370-402/Domain: ankyrin repeat homology <AN11>
F:403-435/Domain: ankyrin repeat homology <AN12>
F:436-468/Domain: ankyrin repeat homology <AN13>
F:469-501/Domain: ankyrin repeat homology <AN14>
F:502-534/Domain: ankyrin repeat homology <AN15>
F:535-567/Domain: ankyrin repeat homology <AN16>
F:568-600/Domain: ankyrin repeat homology <AN17>
F:601-633/Domain: ankyrin repeat homology <AN18>
F:634-666/Domain: ankyrin repeat homology <AN19>
F:667-699/Domain: ankyrin repeat homology <AN20>
F:700-732/Domain: ankyrin repeat homology <AN21>
F:733-765/Domain: ankyrin repeat homology <AN22>
F:766-798/Domain: ankyrin repeat homology <AN23>
F:828-1382/Region: 62K #status predicted <DOM2>
F:828-1382/Domain: spectrin binding
F:1383-1881/Domain: 55K #status predicted <DOM3>

Query Match 8.1%; Score 294; DB 1; Length 1881;
Best Local Similarity 25.6%; Pred. No. 3.2e-14;
Matches 93; Conservative 57; Mismatches 119; Indels 94; Gaps 10;
QY 107 LQHLTDLRNHPSSVAHLAVELGIRECFHH--SRIISCAECAENE---EGCTPLHLACR 161
DB 336 LQHLTFL-----HVA-----HCGHRVAKVLLDKGAKPNSALNGFTPLHIACK 380
QY 162 KGDGEILVELVQVCHTQMD-----VTDYKGET 188
DB 381 KNRVRVM-ELLKLTGASIDAVTESGLTPLHVASFMGHLPIVKNLLQRGASPNVSNVKVET 439
QY 189 VEHYAVQGDNSQVQLGLGRNAVAGNOVNNQGLTPLHLACOLGKQRMVRVLLLCNARCN 248
DB 440 PLHMAARAGHTEVAKYLLQNK-AKVNAKAKDDQTPLHCAARIGHTNNVKLLLENNANPNL 498
QY 249 MGPNGY-----PIHSAMKFSQKCAEMIISM 274
DB 499 ATTAGHTPLHIAAREGHVETVLALLEKEASQACMTKKGFTPLHVAKYKVRVAELLER 558
QY 275 DSSQIHSKDPRYGASPLHWA---KNAEMAPMLLKRCNCNVNSTSSAGNTALHVGVMNRFD 331
DB 559 DAHP--NAAGKNGLTPLHVAHHNLDIVKLLPRGSGSPHSPAWNGYTPPLHIAAKQNVQE 616

QY 332 CAIVLLTHGANADARGEHGNTPHLHAMSNDNVEMIKALIVFGAEVDTPNDFGFTPTFLAS 391
DB 617 VARSLLQYGGSSANAESVQGVTPHLHAAQBGHAEWVALLLSKQANGNKGNSGLTPLHLVA 676
QY 392 KIG 394
DB 677 QEG 679

Search completed: May 26, 2005, 14:20:36
Job time : 22.6667 secs

[illegible]

Db 466 VPABQSAAPHPPFSLERAQPPPIISLNLEQLDLMHISPAKPAFILGSMRDEKTHDHL 525
QY 426 LCLDGGVKGGLIIIIQLLIAEKASGATKDLFDWVAGTSTGGILALAILHKSMAVMRGM 485
Db 526 LCLDGGVKGGLIIIIQLLIAEKASGATKDLFDWVAGTSTGGILALAILHKSMAVMRGM 585
QY 486 YPRMKDEVPRGSRPYESGPLEFLKREGEHTKMTDVRKPKVMTGTLSDROPAPAEHLFR 545
Db 586 YPRMKDEVPRGSRPYESGPLEFLKREGEHTKMTDVRKPKVMTGTLSDROPAPAEHLFR 645
QY 546 NYDAPETVREPRFNQNVNLRPPAQSDDLVRBAARSSGAAPTYFRPNRGFLDGGLLANP 605
Db 646 NYDAPETVREPRFNQNVNLRPPAQSDDLVRBAARSSGAAPTYFRPNRGFLDGGLLANP 705
QY 606 TLDAMTEIHEYNQDLIRKQKQVKKLSIVVSLGTGRSPQVPVTCVDVPRPNPWLAKT 665
Db 706 TLDAMTEIHEYNQDLIRKQKQVKKLSIVVSLGTGRSPQVPVTCVDVPRPNPWLAKT 765
QY 666 VFGAKELGKMVVDCCTDPDGR 686
Db 766 VFGAKELGKMVVDCCTDPDGR 786

RESULT 2
T22327
hypotheical protein F47A4.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22327
R:Mortimore, B.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z19549
A:Accession: T22327
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-1071 <WTL>
A:Cross-references: UNIPROT:Q20500; EMBL:Z49888; PIDN:CAA90061.1; GSPDB:GN00028; CESP:F47A4
A:Experimental source: clone F47A4
C:Genetics:
A:Gene: CESP:F47A4.5
A:Map position: X
A:Introns: 27/1; 59/2; 134/1; 199/2; 402/2; 460/3; 591/3; 634/3; 665/2; 1018/3

Query Match 17.9%; Score 647.5; DB 2; Length 1071;
Best Local Similarity 27.0%; Pred. No. 1.5e-42;
Matches 194; Conservative 126; Mismatches 260; Indels 139; Gaps 20;

QY 69 FRLFOLELEADALVNFPHQYSSQLLPYESSQVLTHTVL----QHLTDLIRNHPWSVAH 124
Db 315 FSLFRATDKKDLMLLHLCDEKSFUTSLDMNTMRADILRSKIEELVQIRLKPHYMH 374
QY 125 LAVELGIRECFHRSRI-----ISCANCAENBEGCTPLHLACRGDGBILVELVQY 174
Db 375 VALATDRDLDFSDGMKTNMETLEPPESQLRCLCHTENCYPVHVALTMDROKIVERLLEL 434
QY 175 CHTQMDVTKGETVETHYAVQGDNSQVLQLGRNAVAG---LNQVNNQGLTPLHLACQLG 231
Db 435 DPTLFCETDKAGNVVHHV---NSSFCAQIIWDRCPASQHFIDERNMQSQSLPNAVSTA 491
QY 232 KOEMVRVLLCNARCNIMGVPGYPHSAKFSQKGAEMIISM-----DSS 277
Db 492 KPLVATFL-----IGKGAKFTRGDRNELFVAMTSKNAQSVVEVVLTDKP 535
QY 278 QIHSQDPYRGASPLHWAKNAEMARMLLKR-----GCNVNSTSAGNTALHVGVMRNRFDCA 333
Db 536 ETANERDALGNASIAHVALYKESINALLNKRVELGLDIDVKNAGETALLPFTTRKPDLL 595
QY 334 IVLLT---HGANADARGEHNTPLHAMS-----KONVEMIKALIVFGAEVTPNDPFGT 385
Db 596 PLLVTLIYAHGANNATDPHGNTALHKSAAALVDAKKISLECVKFLISAGSNPNKINLRGES 655
QY 386 PTFLASKICKQLDLHISPA---RKPATILG-----SMRDE----- 418

Db 656 PRHLAASL-QNQEMLAAILKAAGATRCPKGYGCGRSNCRHDCSSAEDEYEETLOKIRIGNE 714
QY 419 -----KRTDHLCLCGGVKGLIIIIQLLIAEKASGVA 452
Db 715 SDYEKTEFTASEKLNIQDTLQDSRRGKAKVKNLISMDGGGIRGLVIIQTLLIAIEERLGD 774
QY 453 TKDLFDWVAGTSTGGILALAILHKSMAVMRGMFRMKDEYFRG--SRPYESGPLEFLKR 511
Db 775 IFKYPDWSAGYSTGSLIMAGLATGKSLEMOQOYTLKLDKRVDFGIMPYPYDTVQLKEKFIQD 834
QY 512 EFGHEHTKMTDVRKPKVMTGTLSDROPAPAEHLFRNYDAPETVREPRFNQNVNLRPPAOPS 571
Db 835 QFGTGT-WPEIPYPRLMISAVNSEKLPVLEWARYNKPADV-----APEIPK 881
QY 572 DQLVWRAARSSGAAPTYFRPN-GRPLDGLLANPTLDAMTEIHEYNQDLIRKQKQVKK 630
Db 882 EMLPMALRRSTAAPVLPFKPSEDYIDGGIISNNPALDLMSEVHAYNRELQISGRKSDAV 941
QY 631 KLSIVVSLGTGRSPQVPVTCVDVFR--PSNPWELAKTVFGAKELGKMVVDCCTDPDGR 687
Db 942 QMNVLVSEFTG---QIPSTVIETLISIDNSPLQSIKTI---KNLAAMFIDQATASEGAP 994

RESULT 3
T26261
hypotheical protein W07A8.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26261; T26892
R:Baaham, V.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20184
A:Accession: T26261
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-1023 <WTL>
A:Cross-references: UNIPROT:O62398; EMBL:Z82075; PIDN:CAB04932.1; GSPDB:GN00023; CESP:W07A8.2
A:Experimental source: clone W07A8
R:Ainscough, R.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z20281
A:Accession: T26892
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-1023 <WTL>
A:Cross-references: EMBL:AL021489; PIDN:CAA16371.1; GSPDB:GN00023; CESP:W07A8.2
A:Experimental source: clone Y44A6C
C:Genetics:
A:Gene: CESP:W07A8.2
A:Map position: 5
A:Introns: 32/1; 83/2; 155/3; 202/2; 240/3; 264/1; 331/2; 411/1; 479/3; 534/3; 571/2; 701/2

Query Match 17.5%; Score 634.5; DB 2; Length 1023;
Best Local Similarity 24.2%; Pred. No. 1.5e-41;
Matches 187; Conservative 148; Mismatches 287; Indels 151; Gaps 21;

QY 37 RVREGQILIFONTNRTWDCVLPNPRNSQSGFRFLQLELEAD--ALNVFHOYSQLLPF 94
Db 204 RAKEEEL---KNKPLYHLAITLVNENNEKYVMSLFRSHKLDADVVALCERCENPELFRV 260
QY 95 YESSPOV---LHTEVLQHLTDLIRNHPWSVAHLAVELGIRECFH---SRIISCANCAE 148
Db 261 FPKNVNIDKYLHT-----IFHEDRNMTWKSVHISKISGLLEYFENKHEKLLKLYNLIV 315
QY 149 NEEGCTPLHLACRGDGBILVELVOYCHTQMDVTKGETVETHYAVQGDNSQVLQLL--G 206
Db 316 QPEGSLPLMIAVQNTQIETVSWMLDH-CADINILSSEQNVLHVAATASSGDLIKILWET 374
QY 207 RNAVAGLNQVNNQGLTPLHLACQLGQKQBMVRVLLCNARCNIMGPNG-----Y 254
Db 375 KKCETMINQTSNGYTPAVVA-----LINACLNSCQTLRGFGGIGQSSDSTOMAN 424
QY 255 PIHSAMKFSQ--KGCAEMIISMDSSQIHSKODPRYCASPLHWAKNAEMARMLLKR---GCN 309

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:07:29 ; Search time 19.6667 Seconds
(without alignments)
3361.064 Million cell updates/sec

Title: US-10-612-668-21
Perfect score: 3620
Sequence: 1 MQFFGRLVNTFSGVTNLFNS.....GAKELGKMVVDCTDPDGR 687

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3566.5	98.5	851	T12503	hypothetical prote
2	647.5	17.9	1071	T23237	hypothetical prote
3	634.5	17.5	1023	T26261	hypothetical prote
4	332	9.2	3924	S37431	ankyrin 2, neurona
5	324.5	9.0	468	T33857	hypothetical prote
6	324.5	9.0	2039	T15347	ankyrin-related un
7	320	8.8	1549	T13940	ankyrin - fruit fl
8	296	8.2	4377	A55575	ankyrin 3, long ap
9	294.5	8.1	1765	T42714	ankyrin 3, splice
10	294.5	8.1	1940	T42715	ankyrin 3, splice
11	294.5	8.1	1943	T42713	ankyrin 3, splice
12	294.5	8.1	1961	T42716	ankyrin 3, splice
13	294	8.1	1856	B35049	ankyrin 1, erythro
14	294	8.1	1880	A35049	ankyrin 1, erythro
15	294	8.1	1881	1 SHUK	ankyrin 1, erythro
16	285	7.9	1848	D37771	ankyrin, erythrocy
17	285	7.9	1862	I49502	ankyrin - mouse
18	282.5	7.8	397	T46445	hypothetical prote
19	278.5	7.7	1411	S30355	alpha-latroinsecto
20	269.5	7.4	1265	T02131	hypothetical prote
21	268	7.4	456	T24442	hypothetical prote
22	264	7.3	1423	I37275	death-associated p
23	250.5	6.9	1435	T32930	hypothetical prote
24	249	6.9	791	T42691	hypothetical prote
25	244	6.7	247	D84448	probable ankyrin l
26	242.5	6.7	1401	D11527	alpha-latrotoxin p
27	242	6.7	2437	2 AE2149	transmembrane prot
28	239.5	6.6	426	2 AE2149	hypothetical prote
29	235.5	6.5	355	2 E82354	patatin-related pr

30	234.5	6.5	633	2	T27499	hypothetical prote
31	231	6.4	934	1	H71274	probable ankyrin -
32	229.5	6.3	368	2	T18184	ankyrin repeat pro
33	223	6.2	2524	2	A35844	Xotch protein - Af
34	221.5	6.1	907	2	I50404	p50B/p97 (lyt-10)
35	221.5	6.1	1062	2	T14151	inv protein - mous
36	220.5	6.1	1062	2	T30255	inversin - mouse
37	220	6.1	1184	2	T00253	gene Ankhzn protei
38	219	6.0	2531	2	A46019	notch-1 protein -
39	215	5.9	2555	2	A40043	notch protein homo
40	214.5	5.9	2531	2	S18188	notch protein homo
41	213.5	5.9	679	2	J71615	phospholipase A2-1
42	213.5	5.9	782	2	GC7284	phospholipase A2 (
43	213.5	5.9	933	2	SL7233	transcription fact
44	208.5	5.8	606	2	AC2508	hypothetical prote
45	207	5.7	2352	2	T30201	Notch homolog prot

ALIGNMENTS

RESULT 1
T12503
hypothetical protein DKFp434A102.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C:Accession: T12503
R:Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z17527
A:Accession: T12503
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-851 <ANS>
A:Cross-references: EMBL:AL080187
A:Experimental source: adult testis; clone DKFp434A102
C:Genetics:
A:Note: DKFp434A102.1

Query Match	98.5%	Score	3566.5	DB	2	Length	851
Best Local Similarity	92.3%	Pred. No.	1.5e-273				
Matches	684	Conservative	1	Mismatches	1	Indels	55
Gaps	1						
QY	1	MOFFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV	60				
DB	46	MOFFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV	105				
QY	61	NPRNSQSGFRLPQLEADALVNFHQYSSQLLPFYESSPQVLHTEVLQHLTDLIRNHPWS	120				
DB	106	NPRNSQSGFRLPQLEADALVNFHQYSSQLLPFYESSPQVLHTEVLQHLTDLIRNHPWS	165				
QY	121	SVAHLAVELGIRECFHSHRIISCANCAENEECTPLHLACRGDGEILVELVOYCHTQMD	180				
DB	166	SVAHLAVELGIRECFHSHRIISCANCAENEECTPLHLACRGDGEILVELVOYCHTQMD	225				
QY	181	VTDYKGETVFHVAVQGDNSQVLQLGRNAVAGINOVNNOGLTPLHLACQLGQEMVRVLL	240				
DB	226	VTDYKGETVFHVAVQGDNSQVLQLGRNAVAGINOVNNOGLTPLHLACQLGQEMVRVLL	285				
QY	241	LCNARCNIIMPNGYPIHSAMKFSQKGCAPMIISMDSSQIHSKDPDPRYGASPLHWAKNAEMA	300				
DB	286	LCNARCNIIMPNGYPIHSAMKFSQKGCAPMIISMDSSQIHSKDPDPRYGASPLHWAKNAEMA	345				
QY	301	RMLLRKGCNVNSTSAGNTALHVGVMRNFDCAVILLTHGANADARGEHNTPLHLAMSK	360				
DB	346	RMLLRKGCNVNSTSAGNTALHVGVMRNFDCAVILLTHGANADARGEHNTPLHLAMSK	405				
QY	361	DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIGK-----	395				
DB	406	DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIGRLVTRKAILTLRTVGAECYCFPIHG	465				
QY	396	-----LQDLMHISRPKPAFTILGSMRDEKRTDHL	425				

Db	517	HTKMTUVKKVWLTGTLSDRQPAELHLFRNYDAPEVIREPRNQINILKPTQPADQLV	576
Qy	181	WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNODLIRKQANKVKKLSIV	240
Db	577	WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNODMIRKQGNKVKKLSIV	636
Qy	241	VSLGTGRSPQVPVTCVDVFRPNPWELAKTVFGAKELGKMWVDCCTDDPGR	291
Db	637	VSLGTGRSPQVPVTCVDVFRPNPWELAKTVFGAKELGKMWVDCCTDDPGR	687

Search completed: May 26, 2005, 14:21:57
Job time : 11.7676 secs

Query Match		96.1%;	Score 1471;	DB 2;	Length 752;
Best Local Similarity		95.2%;	Pred. No. 3.3e-160;		
Matches		277;	Conservative	8;	Mismatches 6; Indels 0; Gaps 0;
QY	1	LODLMHSRARKPAF	ILGSMRDEK	RTHDLLCLDGGVGKGLII	QLLIIAIEKASGVATKD 60
Db	397	LODLMPISRARKPAF	ILSSMRDEK	RTHDLLCLDGGVGKGLVII	QLLIIAIEKASGVATKD 456
QY	61	LPDWAGTSTGGILAL	AILHKSMA	YMRGMVFRMKDE	VERGSRPYESGPLEFLKREFGE 120
Db	457	LPDWAGTSTGGILAL	AILHKSMA	YMRGMVFRMKDE	VERGSRPYESGPLEFLKREFGE 516
QY	121	HTKMTDVRKPKVMT	GTLSDRQPAEL	HLFRNYDAPETV	REPRFNQNVNLRPPAQPSDQLV 180
Db	517	HTKMTDVRKPKVMT	GTLSDRQPAEL	HLFRNYDAPETV	REPRFNQNVNLRPPAQPSDQLV 576
QY	181	WRAARSSGAAPTY	FRPNRFLDGL	LANNPTLDAMTEI	HEYNQDLIRKGOANKVKLSIV 240
Db	577	WRAARSSGAAPTY	FRPNRFLDGL	LANNPTLDAMTEI	HEYNQDLIRKGOANKVKLSIV 636
QY	241	VSLGTRSPQVPVT	CDVFRPSNP	WELAKTVFGAKEL	GKMVDDCCTDPDGR 291
Db	637	VSLGTRSPQVPVT	CDVFRPSNP	WELAKTVFGAKEL	GKMVDDCCTDPDGR 687
RESULT 14					
US-08-555-5688-2					
; Sequence 2, Application US/085555688					
; Patent No. 5976854					
; GENERAL INFORMATION:					
; APPLICANT: Jones, Simon					
; APPLICANT: Tang, Jim					
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B					
; NUMBER OF SEQUENCES: 25					
; CORRESPONDENCE ADDRESS:					
; ADDRESSEE: Genetics Institute, Inc.					
; STREET: 87 CambridgePark Drive					
; CITY: Cambridge					
; STATE: Massachusetts					
; COUNTRY: U.S.A.					
; ZIP: 02140					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/08/555,568B					
; FILING DATE:					
; CLASSIFICATION: 435					
; ATTORNEY/AGENT INFORMATION:					
; NAME: Brown, Scott A.					
; REGISTRATION NUMBER: 32,724					
; TELECOMMUNICATION INFORMATION:					
; TELEPHONE: (617) 498-8224					
; TELEFAX: (617) 876-5851					
; INFORMATION FOR SEQ ID NO: 2:					
; SEQUENCE CHARACTERISTICS:					
; LENGTH: 752 amino acids					
; TYPE: amino acid					
; TOPOLOGY: linear					
; MOLECULE TYPE: protein					
US-08-555-5688-2					
Query Match		96.1%;	Score 1471;	DB 2;	Length 752;
Best Local Similarity		95.2%;	Pred. No. 3.3e-160;		
Matches		277;	Conservative	8;	Mismatches 6; Indels 0; Gaps 0;
QY	1	LODLMHSRARKPAF	ILGSMRDEK	RTHDLLCLDGGVGKGLII	QLLIIAIEKASGVATKD 60
Db	397	LODLMPISRARKPAF	ILSSMRDEK	RTHDLLCLDGGVGKGLVII	QLLIIAIEKASGVATKD 456
Query Match		96.1%;	Score 1471;	DB 3;	Length 752;
Best Local Similarity		95.2%;	Pred. No. 3.3e-160;		
Matches		277;	Conservative	8;	Mismatches 6; Indels 0; Gaps 0;
QY	1	LODLMHSRARKPAF	ILGSMRDEK	RTHDLLCLDGGVGKGLII	QLLIIAIEKASGVATKD 60
Db	397	LODLMPISRARKPAF	ILSSMRDEK	RTHDLLCLDGGVGKGLVII	QLLIIAIEKASGVATKD 456
QY	61	LPDWAGTSTGGILAL	AILHKSMA	YMRGMVFRMKDE	VERGSRPYESGPLEFLKREFGE 120
Db	457	LPDWAGTSTGGILAL	AILHKSMA	YMRGMVFRMKDE	VERGSRPYESGPLEFLKREFGE 516
QY	121	HTKMTDVRKPKVMT	GTLSDRQPAEL	HLFRNYDAPETV	REPRFNQNVNLRPPAQPSDQLV 180
Db	517	HTKMTDVRKPKVMT	GTLSDRQPAEL	HLFRNYDAPETV	REPRFNQNVNLRPPAQPSDQLV 576
QY	181	WRAARSSGAAPTY	FRPNRFLDGL	LANNPTLDAMTEI	HEYNQDLIRKGOANKVKLSIV 240
Db	577	WRAARSSGAAPTY	FRPNRFLDGL	LANNPTLDAMTEI	HEYNQDLIRKGOANKVKLSIV 636
QY	241	VSLGTRSPQVPVT	CDVFRPSNP	WELAKTVFGAKEL	GKMVDDCCTDPDGR 291
Db	637	VSLGTRSPQVPVT	CDVFRPSNP	WELAKTVFGAKEL	GKMVDDCCTDPDGR 687
RESULT 15					
US-09-519-223-2					
; Sequence 2, Application US/09519223					
; Patent No. 6274140					
; GENERAL INFORMATION:					
; APPLICANT: Jones, Simon					
; APPLICANT: Tang, Jim					
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B					
; NUMBER OF SEQUENCES: 25					
; CORRESPONDENCE ADDRESS:					
; ADDRESSEE: Genetics Institute, Inc.					
; STREET: 87 CambridgePark Drive					
; CITY: Cambridge					
; STATE: Massachusetts					
; COUNTRY: U.S.A.					
; ZIP: 02140					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/09/519,223					
; FILING DATE:					
; CLASSIFICATION:					
; PRIOR APPLICATION NUMBER: US/08/555,568					
; FILING DATE:					
; ATTORNEY/AGENT INFORMATION:					
; NAME: Brown, Scott A.					
; REGISTRATION NUMBER: 32,724					
; TELECOMMUNICATION INFORMATION:					
; TELEPHONE: (617) 498-8224					
; TELEFAX: (617) 876-5851					
; INFORMATION FOR SEQ ID NO: 2:					
; SEQUENCE CHARACTERISTICS:					
; LENGTH: 752 amino acids					
; TYPE: amino acid					
; TOPOLOGY: linear					
; MOLECULE TYPE: protein					
US-09-519-223-2					

QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQSDQLV 180
DB 584 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQSDQLV 643
QY 181 WRAARSSGAAPTYFRPNRGFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240
DB 644 WRAARSSGAAPTYFRPNRGFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 703
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 291
DB 704 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 754

RESULT 11
US-08-281-193-2
; Sequence 2, Application US/08281193
; Patent No. 5466595
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-281-193-2

Query Match 96.1%; Score 1471; DB 1; Length 752;
Best Local Similarity 95.2%; Pred. No. 3.3e-160;
Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 LQDLMHISRARKPAFILSGMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
DB 397 LQDLMPISRARKPAFILSSMRDEKRIHDHLLCLDGGGVKGLVIIQLLIAIEKASGVATKD 456
QY 61 LFDWVAGTSTGGILALAILHKSMSMAYMRGMYFRMKDEVFRGSRPYESGPLEBFLKREFGE 120
DB 457 LFDWVAGTSTGGILALAILHKSMSMAYMRGMYFRMKDEVFRGSRPYESGPLEBFLKREFGE 516
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQSDQLV 180
DB 517 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQSDQLV 576
QY 181 WRAARSSGAAPTYFRPNRGFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240
DB 577 WRAARSSGAAPTYFRPNRGFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 636
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 291
DB 637 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 12
US-08-422-106-2
; Sequence 2, Application US/08422106
; Patent No. 5589170
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,106
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-422-106-2

Query Match 96.1%; Score 1471; DB 1; Length 752;
Best Local Similarity 95.2%; Pred. No. 3.3e-160;
Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 LQDLMHISRARKPAFILSGMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
DB 397 LQDLMPISRARKPAFILSSMRDEKRIHDHLLCLDGGGVKGLVIIQLLIAIEKASGVATKD 456
QY 61 LFDWVAGTSTGGILALAILHKSMSMAYMRGMYFRMKDEVFRGSRPYESGPLEBFLKREFGE 120
DB 457 LFDWVAGTSTGGILALAILHKSMSMAYMRGMYFRMKDEVFRGSRPYESGPLEBFLKREFGE 516
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQSDQLV 180
DB 517 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQSDQLV 576
QY 181 WRAARSSGAAPTYFRPNRGFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240
DB 577 WRAARSSGAAPTYFRPNRGFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 636
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 291
DB 637 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 13
US-08-735-716-2
; Sequence 2, Application US/08735716
; Patent No. 5840511
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,716
; FILING DATE: 23-OCT-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-735-716-2

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; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-519-223-23

Query Match 100.0%; Score 1531; DB 3; Length 688;
Best Local Similarity 100.0%; Pred. No. 3.5e-167;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMHISRARKPAFILGSMRDEKTRTHDLLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
Db 397 LQDLMHISRARKPAFILGSMRDEKTRTHDLLCLDGGGVKGLIIQLLIAIEKASGVATKD 456

QY 61 LFDWAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFKREFGE 120
Db 457 LFDWAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFKREFGE 516

QY 121 HTKMTDVRKPKVMTGLTSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLV 180
Db 517 HTKMTDVRKPKVMTGLTSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLV 576

QY 181 WRAARSSGAAPTYFRPNRGFLDGLLANNPTLDAMTEIHEYNDLLRKQANKVKLSIV 240
Db 577 WRAARSSGAAPTYFRPNRGFLDGLLANNPTLDAMTEIHEYNDLLRKQANKVKLSIV 636

QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVVDCCCTDPDGRP 292
Db 637 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVVDCCCTDPDGRP 688

RESULT 9
US-09-927-180-23
; Sequence 23, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TANG, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-927-180-23

Query Match 100.0%; Score 1531; DB 4; Length 688;
Best Local Similarity 100.0%; Pred. No. 3.5e-167;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMHISRARKPAFILGSMRDEKTRTHDLLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
Db 397 LQDLMHISRARKPAFILGSMRDEKTRTHDLLCLDGGGVKGLIIQLLIAIEKASGVATKD 456

QY 61 LFDWAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFKREFGE 120
Db 457 LFDWAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFKREFGE 516

QY 121 HTKMTDVRKPKVMTGLTSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLV 180
Db 517 HTKMTDVRKPKVMTGLTSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLV 576

QY 181 WRAARSSGAAPTYFRPNRGFLDGLLANNPTLDAMTEIHEYNDLLRKQANKVKLSIV 240
Db 577 WRAARSSGAAPTYFRPNRGFLDGLLANNPTLDAMTEIHEYNDLLRKQANKVKLSIV 636

QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVVDCCCTDPDGRP 292
Db 637 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVVDCCCTDPDGRP 688
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RESULT 10
US-09-949-016-10948
; Sequence 10948, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10948
; LENGTH: 819
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10948
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Query Match 99.5%; Score 1524; DB 4; Length 819;
Best Local Similarity 100.0%; Pred. No. 2.9e-166;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMHISRARKPAFILGSMRDEKTRTHDLLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
Db 464 LQDLMHISRARKPAFILGSMRDEKTRTHDLLCLDGGGVKGLIIQLLIAIEKASGVATKD 523

QY 61 LFDWAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFKREFGE 120
Db 524 LFDWAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFKREFGE 583
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;
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 09-Aug-2001
; APPLICATION NUMBER: US/09/927,180
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match 100.0%; Score 1531; DB 4; Length 687;
Best Local Similarity 100.0%; Pred. No. 3.5e-167;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMHISRRKPAFLGSMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
Db |||||
QY 396 LQDLMHISRRKPAFLGSMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 455
Db |||||
QY 61 LFDWAGTGTGILALAILHKSMAVMRGYFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
Db |||||
QY 456 LFDWAGTGTGILALAILHKSMAVMRGYFRMKDEVFRGSRPYESGPLEEFLKREFGE 515
Db |||||
QY 121 HTKMTDVRKPKVMTGLTSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQIV 180
Db |||||
QY 516 HTKMTDVRKPKVMTGLTSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQIV 575
Db |||||
QY 181 WRAARSSGAAPTYFRPNRFLDGLGGLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240
Db |||||
QY 576 WRAARSSGAAPTYFRPNRFLDGLGGLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 635
Db |||||
QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGMVVDCCCTDDPGRP 292
Db |||||
QY 636 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGMVVDCCCTDDPGRP 687
Db |||||

RESULT 7
US-08-555-568B-23
; Sequence 23, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:

;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-555-568B-23

Query Match 100.0%; Score 1531; DB 2; Length 688;
Best Local Similarity 100.0%; Pred. No. 3.5e-167;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMHISRRKPAFLGSMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
Db |||||
QY 397 LQDLMHISRRKPAFLGSMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 456
Db |||||
QY 61 LFDWAGTGTGILALAILHKSMAVMRGYFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
Db |||||
QY 457 LFDWAGTGTGILALAILHKSMAVMRGYFRMKDEVFRGSRPYESGPLEEFLKREFGE 516
Db |||||
QY 121 HTKMTDVRKPKVMTGLTSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQIV 180
Db |||||
QY 517 HTKMTDVRKPKVMTGLTSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQIV 576
Db |||||
QY 181 WRAARSSGAAPTYFRPNRFLDGLGGLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240
Db |||||
QY 577 WRAARSSGAAPTYFRPNRFLDGLGGLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 636
Db |||||
QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGMVVDCCCTDDPGRP 292
Db |||||
QY 637 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGMVVDCCCTDDPGRP 688
Db |||||

RESULT 8
US-09-519-223-23
; Sequence 23, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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QY 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDMATEIHEYNDLIRKQANKVKLSIV 240
DB 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDMATEIHEYNDLIRKQANKVKLSIV 240
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGRP 292
DB 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGRP 292

RESULT 2

US-09-519-223-19
; Sequence 19, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 292 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-519-223-19

Query Match 100.0%; Score 1531; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 9.1e-168;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMHISRAKPAFILGSMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
DB 1 LQDLMHISRAKPAFILGSMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
QY 61 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEEFKKEFGE 120
DB 61 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEEFKKEFGE 120
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQVNLRRPPAQPSDQLV 180
DB 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQVNLRRPPAQPSDQLV 180
QY 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDMATEIHEYNDLIRKQANKVKLSIV 240
DB 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDMATEIHEYNDLIRKQANKVKLSIV 240

QY 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDMATEIHEYNDLIRKQANKVKLSIV 240

DB 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDMATEIHEYNDLIRKQANKVKLSIV 240
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGRP 292
DB 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGRP 292

RESULT 3

US-09-927-180-19
; Sequence 19, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 292 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-927-180-19

Query Match 100.0%; Score 1531; DB 4; Length 292;
Best Local Similarity 100.0%; Pred. No. 9.1e-168;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 LQDLMHISRAKPAFILGSMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
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DB 61 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEEFKKEFGE 120
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQVNLRRPPAQPSDQLV 180
DB 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQVNLRRPPAQPSDQLV 180
QY 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDMATEIHEYNDLIRKQANKVKLSIV 240
DB 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDMATEIHEYNDLIRKQANKVKLSIV 240
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGRP 292

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:08:24 ; Search time 10.7676 seconds
(without alignments)
2024.365 Million cell updates/sec

Title: US-10-612-668-19

Perfect score: 1531

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1531	100.0	292	3	US-09-519-223-19
3	1531	100.0	292	4	US-09-927-180-19
4	1531	100.0	687	2	US-08-555-568B-21
5	1531	100.0	687	3	US-09-519-223-21
6	1531	100.0	687	4	US-09-927-180-21
7	1531	100.0	688	2	US-08-555-568B-23
8	1531	100.0	688	3	US-09-519-223-23
9	1531	100.0	688	4	US-09-927-180-23
10	1524	99.5	819	4	US-09-949-016-10948
11	1471	96.1	752	1	US-08-281-193-2
12	1471	96.1	752	1	US-08-422-106-2
13	1471	96.1	752	2	US-08-735-716-2
14	1471	96.1	752	2	US-08-555-568B-2
15	1471	96.1	752	3	US-09-519-223-2
16	1471	96.1	752	4	US-09-927-180-2
17	1471	96.1	752	5	PCT-US95-08069-2
18	736	48.1	896	4	US-09-270-767-46130
19	610	39.8	545	4	US-09-270-767-61684
20	371	24.2	143	4	US-09-270-767-33298
21	177	11.6	410	4	US-09-755-630B-290
22	177	11.6	410	4	US-09-755-630B-292
23	177	11.6	410	4	US-09-755-274-10
24	177	11.6	410	4	US-09-755-274-12
25	175	11.4	337	4	US-09-755-630B-293
26	175	11.4	337	4	US-09-755-274-13
27	175	11.4	410	2	US-08-449-986-2

28	175	11.4	410	2	US-08-756-855-2	Sequence 2, Appli
29	175	11.4	410	4	US-09-755-630B-288	Sequence 288, App
30	175	11.4	410	4	US-09-755-630B-291	Sequence 291, App
31	175	11.4	410	4	US-09-755-274-8	Sequence 8, Appli
32	175	11.4	410	4	US-09-755-274-11	Sequence 11, Appli
33	175	11.4	508	4	US-09-755-630B-289	Sequence 289, App
34	175	11.4	508	4	US-09-755-274-9	Sequence 9, Appli
35	142.5	9.3	383	1	US-07-936-163-4	Sequence 4, Appli
36	140	9.1	381	1	US-07-936-163-3	Sequence 3, Appli
37	140	9.1	386	4	US-09-755-630B-278	Sequence 278, App
38	140	9.1	386	4	US-09-755-274-5	Sequence 5, Appli
39	139	9.1	366	4	US-09-755-630B-263	Sequence 263, App
40	139	9.1	366	4	US-09-755-274-29	Sequence 29, Appli
41	138	9.0	367	4	US-09-755-630B-7	Sequence 7, Appli
42	138	9.0	367	4	US-09-755-274-41	Sequence 41, Appli
43	138	9.0	386	4	US-09-755-630B-2	Sequence 2, Appli
44	138	9.0	386	4	US-09-755-630B-265	Sequence 265, App
45	138	9.0	386	4	US-09-755-630B-286	Sequence 286, App

ALIGNMENTS

RESULT 1
US-08-555-568B-19
; Sequence 19, Application US/085555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 292 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-19

Query Match 100.0%; Score 1531; DB 2; Length 292;
Best Local Similarity 100.0%; Pred. No. 9.1e-168;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	LQDLMHISRKPAFILGSMRDEKTRHLLCLDGGVKGKLIILQLLIAIEKASGVATKD	60
QY	61	LFDWAGTGTGGILALAILHKSMAVMGMGMKDEVRGSRPYSGPLEFLKRFGE	120
Db	61	LFDWAGTGTGGILALAILHKSMAVMGMGMKDEVRGSRPYSGPLEFLKRFGE	120

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Db      380 KMWQAIRASSAAGFYAEYALGNDLHQDGGLLNNPSALAMHECKCLWPDV----- 430
Qy      235 KKLIVVSLGTGR 247
Db      431 -PLECIVSLGTGR 442
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RESULT 15
US-10-786-505-18
; Sequence 18, Application US/10786505
; Publication No. US20050003388A1
; GENERAL INFORMATION:
; APPLICANT: GROSS, RICHARD W.
; APPLICANT: DAVID J. MANCUSO
; TITLE OF INVENTION: CALCIUM INDEPENDENT PHOSPHOLIPASE A2V POLYNUCLEOTIDES
; TITLE OF INVENTION: AND POLYPEPTIDES AND METHODS THEREFOR
; FILE REFERENCE: 15060-58
; CURRENT APPLICATION NUMBER: US/10/786,505
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: 09/168,623
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 18
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-786-505-18
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Best Local Similarity 28.5%; Pred. No. 8.3e-13;
Matches 72; Conservative 33; Mismatches 107; Indels 41; Gaps 8;

Qy      16 ILGSMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILA 75
Db      309 LIGYDVPKRGIRILSIDGGGTRGVVALQTLRKLVELTQKPVHQLFDYICGVSTGAILA 368

Qy      76 LAI-LHSKSMAYMRGMVFRMKDVER-----GSRPVESGPLEEFLKREFGEHT 122
Db      369 FMLGLFHPMLDECEELYRLKLGSDVFSQNVIVGTVMKWSHAFYDSQTSWENILKDRMGSA 428

Qy      123 KMTDVRK---PKVMLTGTLSDRQ-PAELHLFRNYDAPETVREFRNQNVNLRPPAQPDSQ 178
Db      429 MIETARNPTCPKVAAVSTIVNRGITPKAFVFRNYG-----HPPGINSHY-----LGGCQY 478

Qy      179 LVWRAARSSGAAPTYFRP-----NGREFDGLLANPTLDAMTEIHEYNQOOLIRKQANKV 234
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; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4998
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-4998

Query Match      17.0%; Score 261; DB 15; Length 468;
Best Local Similarity 29.8%; Pred. No. 3.1e-18;
Matches 78; Conservative 54; Mismatches 100; Indels 30; Gaps 10;

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DB 180 VLASEKKQKWPPEVRVIALDGGIRAVITIQMLIHIDYLLGGKLVKELDDIAGTSCGGEVI 239

QY 75 ALAI-LHKSMAVMRGMYFRMKDEVF-RGSR---PYESGPLEEFLKREF--GEHTKMTDV 127
DB 240 TLLSTNNRNIETBKLLDMDRDFIRGADKAVPKYSNGMEYIARHVTWEDSKMSSI 299

QY 128 RKPVMLTGTLSDRQPAELHLFRNY--DAPETVREP-RFNQVNLRRPPAQPSDOLVWRAA 184
DB 300 KRHRATVTVADTRMVPQQLLFRSYRPEMPEACEHYKF-----LDPTKVELWKTL 350

QY 185 RSSGAAPTFRPNRFLDGLLANNPTLDMATEIHEYNDLIRKQANKVK-----K 236
DB 351 RCTTAAPYFPFESNGSLDGLIANNPTLALISDFLTKN--LEKSFASKSSERENRGWK 408

QY 237 LSIWVSLGTGRSPQVPVTCVDV 258
DB 409 IGCVISLGTGVPTXKIDGL 430

RESULT 10
US-10-437-963-169583
; Sequence 169583, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 169583
; LENGTH: 1254
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_67990C.1.pep
US-10-437-963-169583

Query Match      15.3%; Score 235; DB 16; Length 1254;
Best Local Similarity 25.9%; Pred. No. 7.2e-15;
Matches 89; Conservative 48; Mismatches 101; Indels 106; Gaps 15;

QY 1 LODLM-----HISRAKPAF-ILGSMRDEKTHD-----HLLCLDGGGVKGL 41
DB 487 LRDLIRLTLSEKRVKAAALALGLENLRRAIRGRPVAKKGLRILSMDDGGKGL 546
QY 42 IITQLLIAIEKASGVATKDLFDWAGTSTGGILALAI-LHKSMAVMRGMYFRM----- 94

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QY 1 LQDLMIHSRARKPAFILGSMRDEKTRHDHLLCLDGGGVKGLIIQLIIAIEKASGVATKD 60
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QY 61 LFDWVAGTSTGGILALAILHSKSMAYMRGMYFRMKDEVFRGSRPYSGPLEEFLKREFGE 120
DB 457 LFDWVAGTSTGGILALAILHSKSMAYMRGMYFRMKDEVFRGSRPYSGPLEEFLKREFGE 516
QY 121 HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQLV 180
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QY 181 WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNDLIRKGOANKVKKLSIV 240
DB 577 WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNDLIRKGOANKVKKLSIV 636
QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVDDCCTDPDGR 292
DB 637 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVDDCCTDPDGR 688

RESULT 4

US-10-108-260A-3778
; Sequence 3778, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cdna
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3778
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3778

Query Match 99.5%; Score 1524; DB 15; Length 667;
Best Local Similarity 100.0%; Pred. No. 5.9e-151;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 372 LFDWVAGTSTGGILALAILHSKSMAYMRGMYFRMKDEVFRGSRPYSGPLEEFLKREFGE 431
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DB 432 HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQLV 491
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DB 492 WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNDLIRKGOANKVKKLSIV 551
QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVDDCCTDPDGR 291
DB 552 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVDDCCTDPDGR 602

RESULT 5

US-09-927-180-2
; Sequence 2, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-927-180-2

Query Match 96.1%; Score 1471; DB 9; Length 752;
Best Local Similarity 95.2%; Pred. No. 2.7e-145;
Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
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DB 397 LQDLMIHSRARKPAFILGSMRDEKTRHDHLLCLDGGGVKGLIIQLIIAIEKASGVATKD 456
QY 61 LFDWVAGTSTGGILALAILHSKSMAYMRGMYFRMKDEVFRGSRPYSGPLEEFLKREFGE 120
DB 457 LFDWVAGTSTGGILALAILHSKSMAYMRGMYFRMKDEVFRGSRPYSGPLEEFLKREFGE 516
QY 121 HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQLV 180
DB 517 HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQLV 576
QY 181 WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNDLIRKGOANKVKKLSIV 240
DB 577 WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNDLIRKGOANKVKKLSIV 636
QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVDDCCTDPDGR 291
DB 637 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVDDCCTDPDGR 687

RESULT 6

US-10-369-493-6865
; Sequence 6865, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B

```

;
; LENGTH: 292 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-927-180-19

Query Match 100.0%; Score 1531; DB 9; Length 292;
Best Local Similarity 100.0%; Pred. No. 3.2e-152;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMHISRARKPAFLTSGMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
DB 1 LQDLMHISRARKPAFLTSGMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
QY 61 LFDWVAGTSTGGILALAILHSHSKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
DB 61 LFDWVAGTSTGGILALAILHSHSKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQV 180
DB 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQV 180
QY 181 WRAARSSGAAPTYFRPNRFLDGGILLANNPTLDAMTEIHEYNQDLIRKGQANKVKKLSIV 240
DB 181 WRAARSSGAAPTYFRPNRFLDGGILLANNPTLDAMTEIHEYNQDLIRKGQANKVKKLSIV 240
QY 241 VSLGTRSPQVPVTCVDVFRPNPWEAKTVFGAKELGKMVVDCTDPPDGRP 292
DB 241 VSLGTRSPQVPVTCVDVFRPNPWEAKTVFGAKELGKMVVDCTDPPDGRP 292

RESULT 2
US-09-927-180-21
; Sequence 21, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match 100.0%; Score 1531; DB 9; Length 687;
Best Local Similarity 100.0%; Pred. No. 1.1e-151;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMHISRARKPAFLTSGMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
DB 1 LQDLMHISRARKPAFLTSGMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
QY 61 LFDWVAGTSTGGILALAILHSHSKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
DB 61 LFDWVAGTSTGGILALAILHSHSKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQV 180
DB 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQV 180
QY 181 WRAARSSGAAPTYFRPNRFLDGGILLANNPTLDAMTEIHEYNQDLIRKGQANKVKKLSIV 240
DB 181 WRAARSSGAAPTYFRPNRFLDGGILLANNPTLDAMTEIHEYNQDLIRKGQANKVKKLSIV 240
QY 241 VSLGTRSPQVPVTCVDVFRPNPWEAKTVFGAKELGKMVVDCTDPPDGRP 292
DB 241 VSLGTRSPQVPVTCVDVFRPNPWEAKTVFGAKELGKMVVDCTDPPDGRP 292

RESULT 3
US-09-927-180-23
; Sequence 23, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-927-180-23

Query Match 100.0%; Score 1531; DB 9; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.1e-151;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:20:02 ; Search time 39.8117 Seconds
(without alignments)
2530.207 Million cell updates/sec

Title: US-10-612-668-19

Perfect score: 1531

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1462099

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1531	100.0	292	9 US-09-927-180-19	Sequence 19, Appl
2	1531	100.0	687	9 US-09-927-180-21	Sequence 21, Appl
3	1531	100.0	688	9 US-09-927-180-23	Sequence 23, Appl
4	1524	99.5	667	15 US-10-108-260A-3778	Sequence 3778, Ap
5	1471	96.1	752	9 US-09-927-180-2	Sequence 2, Appl
6	456.5	29.8	1071	15 US-10-369-493-6865	Sequence 6865, Ap
7	419	27.4	1023	15 US-10-369-493-6689	Sequence 6689, Ap
8	419	27.4	1023	15 US-10-369-493-6690	Sequence 6690, Ap
9	261	17.0	1468	15 US-10-369-493-4998	Sequence 4998, Ap
10	235	15.3	1254	16 US-10-437-963-169583	Sequence 169583,
11	234	15.3	387	15 US-10-421-654-66	Sequence 66, Appl
12	234	15.3	387	17 US-10-796-907-66	Sequence 66, Appl
13	211.5	13.8	370	9 US-09-925-300-1483	Sequence 1483, Ap

14	211.5	13.8	562	16	US-10-786-505-21	Sequence 21, Appl
15	211.5	13.8	661	16	US-10-786-505-18	Sequence 18, Appl
16	211.5	13.8	682	16	US-10-786-505-15	Sequence 15, Appl
17	211.5	13.8	782	16	US-10-786-505-1	Sequence 1, Appl
18	208.5	13.6	350	15	US-10-421-654-100	Sequence 100, App
19	208.5	13.6	350	17	US-10-796-907-132	Sequence 132, App
20	207.5	13.6	308	17	US-10-796-907-132	Sequence 132, App
21	204.5	13.4	577	15	US-10-310-154-616	Sequence 616, App
22	201	13.1	315	15	US-10-424-599-259117	Sequence 259117,
23	201	13.1	382	15	US-10-310-154-615	Sequence 615, App
24	195.5	12.8	382	15	US-10-424-599-258423	Sequence 258423,
25	193.5	12.6	387	16	US-10-437-963-177823	Sequence 177823,
26	190	12.4	378	15	US-10-421-654-18	Sequence 18, Appl
27	190	12.4	378	17	US-10-796-907-18	Sequence 18, Appl
28	177	11.6	410	10	US-09-755-630A-290	Sequence 290, App
29	177	11.6	410	10	US-09-755-630A-292	Sequence 292, App
30	177	11.6	434	15	US-10-425-114-39447	Sequence 39447, A
31	177	11.6	437	15	US-10-425-114-39376	Sequence 39376, A
32	177	11.6	439	15	US-10-425-114-47375	Sequence 47375, A
33	177	11.6	441	15	US-10-425-114-57061	Sequence 57061, A
34	177	11.6	442	16	US-10-437-963-138254	Sequence 138254,
35	176	11.5	438	15	US-10-425-114-72032	Sequence 72032, A
36	176	11.5	438	15	US-10-425-114-72035	Sequence 72035, A
37	176	11.5	448	15	US-10-425-114-65072	Sequence 65072, A
38	175	11.4	337	10	US-09-755-630A-293	Sequence 293, App
39	175	11.4	410	10	US-09-755-630A-288	Sequence 288, App
40	175	11.4	410	10	US-09-755-630A-291	Sequence 291, App
41	175	11.4	436	15	US-10-425-114-39450	Sequence 39450, A
42	175	11.4	436	15	US-10-425-114-47374	Sequence 47374, A
43	175	11.4	508	10	US-09-755-630A-289	Sequence 289, App
44	174.5	11.4	405	16	US-10-437-963-129647	Sequence 129647,
45	174	11.4	463	15	US-10-424-599-242149	Sequence 242149,

ALIGNMENTS

RESULT 1

US-09-927-180-19
; Sequence 19, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
;

XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
 XX Homo sapiens.
 OS WO2004023973-A2.
 XX
 XX '25-MAR-2004.
 PD
 XX
 XX 12-SEP-2003; 2003WO-US028227.
 PF
 XX 12-SEP-2002; 2002US-0410259P.
 PR
 XX 12-SEP-2002; 2002US-0410260P.
 PR
 XX (INCY-) INCYTE CORP.
 PA
 XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 PI Harthehorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV;
 PI Mooney EM, Deleagane AM, Panesar IS, Bannville SC, Reddy IP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patury S, Shi X, Suarez CJ;
 XX
 DR WPI; 2004-329368/30.
 DR N-PSDB; ACN43006.
 XX
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX
 XX Claim 27; Page; 190pp; English.
 PS
 XX The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC polynucleotide and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX
 XX Sequence 810 AA;
 SQ
 Query Match 97.9%; Score 1499; DB 8; Length 810;
 Best Local Similarity 90.7%; Pred. No. 5.7e-159;
 Matches 291; Conservative 0; Mismatches 0; Indels 30; Gaps 1;
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 DB 485 LFDWVAGTGTGILALAILHKSMAVMRGMYFRMKDEVRGSRPYESGPLEBFLKREFGE 544
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 DB 605 NYDAPETVREPRFNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFRNGRFLDGLLANNP 664

QY 211 TLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDFRPSNPWELAKT 270
 DB 665 TLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDFRPSNPWELAKT 724
 QY 271 VFGAKELGKMVVDCCTDPDGR 291
 DB 725 VFGAKELGKMVVDCCTDPDGR 745
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 AC AAR83018;
 XX
 DT 15-JUN-1996 (first entry)
 XX
 DE Calcium-independent cytosolic phospholipase-A2/B enzyme.
 XX
 KW CHO; calcium-independent cytosolic phospholipase-A2/B; enzyme;
 KW phospholipase-A2; phospholipase-B; drug screening; antiinflammatory;
 KW antibody.
 XX
 OS Cricetulus griseus.
 XX
 PN US5466595-A.
 XX
 PD 14-NOV-1995.
 XX
 PF 27-JUL-1994; 94US-00281193.
 XX
 PR 27-JUL-1994; 94US-00281193.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Tang J, Jones S;
 XX
 DR WPI; 1996-009526/01.
 DR N-PSDB; AAT05842.
 XX
 PT Isolated polynucleotide encoding cytosolic phospholipase A2/B - for
 PT producing enzyme for use in screening anti-inflammatory agents and prodn.
 PT of antibodies.
 XX
 PS Claim 5; Col 15-22; 24pp; English.
 XX
 CC The enzyme may be produced recombinantly in host cells such as animal
 CC cells, insect cells, eukaryotes, prokaryotes, etc. The protein may also
 CC be expressed in transgenic animals (e.g. milk of transgenic cow). The
 CC protein is used to screen for agents which inhibit phospholipase activity
 CC for use as antiinflammatory agents. These agents can be used to treat
 CC e.g. rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease
 CC and other disease mediated by increased levels of prostaglandins,
 CC leukotriene or platelet activating factor. The enzyme can also be used
 CC for the production of antibodies for use as research or diagnostic tools
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 XX Sequence 752 AA;
 SQ
 Query Match 96.1%; Score 1471; DB 2; Length 752;
 Best Local Similarity 95.2%; Pred. No. 7.3e-156;
 Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
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 QY 61 LFDWVAGTGTGILALAILHKSMAVMRGMYFRMKDEVRGSRPYESGPLEBFLKREFGE 120
 DB 457 LFDWVAGTGTGILALAILHKSMAVMRGMYFRMKDEVRGSRPYESGPLEBFLKREFGE 516
 QY 121 HTKMTDVRKPKVNLTGTLSDROPAPLHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQDLV 180
 DB 605 NYDAPETVREPRFNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFRNGRFLDGLLANNP 664

PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthropathy.
 PI Claim 7; SEQ ID NO 700; 1731pp; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polynuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polynuropathy. This sequence represents a human PRO polypeptide of the
 CC invention.
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 SQ Sequence 806 AA;
 Query Match 99.5%; Score 1524; DB 8; Length 806;
 Best Local Similarity 100.0%; Pred. No. 8.7e-162;
 Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 511 LFDWAGTGTGGILALAILHLSKSMAYMRGMVFRMKDEVERGSRPYSGPLEEFLKREFGE 570
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 Db 631 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 690
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 Db 691 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKVMVDCCTDPDGR 741
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 ID ABM84355 standard; protein; 810 AA.
 AC ABM84355;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4604.
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 KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
 XX
 OS Homo sapiens.
 XX
 PN WO2004023973-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 12-SEP-2003; 2003WO-US028227.
 XX
 PR 12-SEP-2002; 2002US-0410259P.
 PR 12-SEP-2002; 2002US-0410260P.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Eider LV;
 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtan ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Fatury S, Shi X, Suarez CU;
 XX
 DR WPI; 2004-329368/30.
 DR N-PSDB; ACN43007.
 XX
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX
 PS Claim 27; Page; 190pp; English.
 XX
 CC The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX
 SQ Sequence 810 AA;
 Query Match 97.9%; Score 1499; DB 8; Length 810;
 Best Local Similarity 90.7%; Pred. No. 5.7e-159;
 Matches 291; Conservative 0; Mismatches 0; Indels 30; Gaps 1;
 QY 1 LQDLMHISRARKPAFILGSMRDEKTRTHDHLCLDGGGVKGLIIQLIIAIEKASGVATKD 60
 Db 425 LQDLMHISRARKPAFILGSMRDEKTRTHDHLCLDGGGVKGLIIQLIIAIEKASGVATKD 484
 QY 61 LFDWAGTGTGGILALAILHLSKSMAYMRGMVFRMKDEVERGSRPYSGPLEEFLKREFGE 120
 Db 485 LFDWAGTGTGGILALAILHLSKSMAYMRGMVFRMKDEVERGSRPYSGPLEEFLKREFGE 544
 QY 121 HTKMTDVRKPK-----VMTGTLSDRQPAELHLP 150
 Db 545 HTKMTDVRKPKLDQSDTPPALPERACFAGMVRGEAHLSTRTEVMTGLSDRQPAELHLP 604
 QY 151 NYDAPETVREPRENQNVNLRPPAQSOLVWRAARSSGAAPTYFRPNRFLDGLLANNP 210
 Db 605 NYDAPETVREPRENQNVNLRPPAQSOLVWRAARSSGAAPTYFRPNRFLDGLLANNP 664
 QY 211 TLDAMTEIHEYNDLIRKQANKVKLSIVVSLGTRSPQVPVTCVDVFRPSNPWELAKT 270
 Db 665 TLDAMTEIHEYNDLIRKQANKVKLSIVVSLGTRSPQVPVTCVDVFRPSNPWELAKT 724
 QY 271 VFGAKELGKVMVDCCTDPDGR 291
 Db 725 VFGAKELGKVMVDCCTDPDGR 745
 RESULT 12
 ABM84354
 ID ABM84354 standard; protein; 810 AA.
 XX
 AC ABM84354;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4603.

CC atherosclerosis), or hepatic diseases (e.g. cirrhosis). The invention
CC also relates to the assessment of the effects of exogenous compounds on
CC the expression of nucleic acids and LipAms. The invention provides
CC expression vectors, host cells, antibodies, agonists and antagonists,
CC transgenic organisms, and arrays and microarrays of the polynucleotides.
XX
SQ Sequence 784 AA;

Query Match 99.5%; Score 1524; DB 7; Length 784;
Best Local Similarity 100.0%; Pred. No. 8.3e-162;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LODLHHSRARKPAFTLGSMDKRTDHLCLDGGVKGGLIIIOILLIAIEKASGVATKD 60
Db 429 LODLHHSRARKPAFTLGSMDKRTDHLCLDGGVKGGLIIIOILLIAIEKASGVATKD 488
QY 61 LFDWVAGTSTGGILALAILHKSMAVMRGMYFRMKDEVERGSRPYESGPLEEFLKREFGE 120
Db 489 LFDWVAGTSTGGILALAILHKSMAVMRGMYFRMKDEVERGSRPYESGPLEEFLKREFGE 548
QY 121 HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQIV 180
Db 549 HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQIV 608
QY 181 WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNODLIRKQANKVKLSIV 240
Db 609 WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNODLIRKQANKVKLSIV 668
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR 291
Db 669 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR 719

RESULT 9
AAE25968
ID AAE25968 standard; protein; 806 AA.
XX
AC AAE25968;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human PLA2 group VI (Ca2+-independent) protein.
XX
KW Human; antisense; phospholipase A2; infection; inflammation; tumour;
KW antisense therapy; PLA2 protein.
XX
OS Homo sapiens.
XX
PN US6410325-B1.
XX
PD 25-JUN-2002.
XX
PF 09-MAY-2001; 2001US-00851896.
XX
PR 09-MAY-2001; 2001US-00851896.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Freier SM, Watt AT;
XX
DR WPI; 2002-616513/66.
XX
DR N-PSDB; AAD42941.

PT Novel antisense compounds useful for inhibiting gene expression of human
PT phospholipase A2, group VI and for treating diseases associated with
PT expression of phospholipase A2, group VI.
XX
PS Disclosure; Col 109-116; 72pp; English.
XX
CC The present invention relates to novel antisense compounds which inhibit
CC the expression of phospholipase A2 (PLA2), group VI (Ca2+-independent).
CC The invention is useful for inhibiting the expression of PLA2, group VI
CC (Ca2+-independent) in human cells or tissues and for treating an animal,

CC particularly a human suspected of having or being prone to a disease or
CC condition associated with expression of human PLA2, group VI (Ca2+-
CC independent). It is useful for diagnostics, therapeutics and as research
CC reagent, e.g. prophylactically to prevent or delay infection, tumour
CC formation or inflammation. The present sequence is human PLA2 group VI
CC (Ca2+-independent) protein
XX
SQ Sequence 806 AA;

Query Match 99.5%; Score 1524; DB 5; Length 806;
Best Local Similarity 100.0%; Pred. No. 8.7e-162;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LODLHHSRARKPAFTLGSMDKRTDHLCLDGGVKGGLIIIOILLIAIEKASGVATKD 60
Db 451 LODLHHSRARKPAFTLGSMDKRTDHLCLDGGVKGGLIIIOILLIAIEKASGVATKD 510
QY 61 LFDWVAGTSTGGILALAILHKSMAVMRGMYFRMKDEVERGSRPYESGPLEEFLKREFGE 120
Db 511 LFDWVAGTSTGGILALAILHKSMAVMRGMYFRMKDEVERGSRPYESGPLEEFLKREFGE 570
QY 121 HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQIV 180
Db 571 HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQIV 630
QY 181 WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNODLIRKQANKVKLSIV 240
Db 631 WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNODLIRKQANKVKLSIV 690
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR 291
Db 691 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR 741

RESULT 10
ADO19776
ID ADO19776 standard; protein; 806 AA.
XX
AC ADO19776;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human PRO polypeptide #350.
XX
KW Human; PRO; immune related disorder; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
KW diabetes mellitus; renal disease; demyelinating disease;
KW central nervous system; peripheral nervous system;
KW demyelinating polyneuropathy; Guillain-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy.
XX
OS Homo sapiens.
XX
PN WO2004043361-A2.
XX
PD 27-MAY-2004.
XX
PF 06-NOV-2003; 2003WO-US035268.
XX
PR 08-NOV-2002; 2002US-0425235P.
XX
PA (GETH) GENENTECH INC.
XX
PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
XX
DR WPI; 2004-420067/39.
XX
DR N-PSDB; ADO19775.
XX
PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
PT treating an immune related disorder such as systemic lupus erythematosus,

Db 577 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKGOANKVKLSIV 636
QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCDDPDGRP 292
Db 637 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCDDPDGRP 688
RESULT 7
ADM05093
ID ADM05093 standard; protein; 667 AA.
AC ADM05093;
XX
DT 20-MAY-2004 (first entry)
DE Human protein of the invention SEQ ID NO:3778.
XX
KW human; gene therapy; diagnostic marker; pharmaceutical.
XX
OS Homo sapiens.
XX
PN EP1347046-A1.
XX
XX 24-SEP-2003.
XX
PF 12-APR-2002; 2002EP-00008400.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuka T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-723558/69.
DR N-PSDB; ADM02650.
XX
PT New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
PS Claim 1; SEQ ID NO 3778; 305pp; English.
XX
CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM03116-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.
XX
SQ Sequence 667 AA;

Query Match 99.5%; Score 1524; DB 7; Length 667;
Best Local Similarity 100.0%; Pred. No. 6.5e-162;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMHISRKAPAFILGSMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
Db 312 LQDLMHISRKAPAFILGSMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 371
QY 61 LFDWVAGTGTGILALAILHKSMAWYMRGMVFRMKDEVFRGSRPYBSGPLEBFLKEEFG 120
Db 372 LFDWVAGTGTGILALAILHKSMAWYMRGMVFRMKDEVFRGSRPYBSGPLEBFLKEEFG 431
QY 121 HTKMTDVRKPKVMLTGLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180
Db 432 HTKMTDVRKPKVMLTGLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 491

QY 181 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKGOANKVKLSIV 240
Db 492 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKGOANKVKLSIV 551
QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCDDPDGR 291
Db 552 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCDDPDGR 602
RESULT 8
ADD93407
ID ADD93407 standard; protein; 784 AA.
XX
AC ADD93407;
XX
DT 29-JAN-2004 (first entry)
DE Human lipid-associated molecule LIPAM-14 polypeptide.
XX
KW Human; lipid-associated molecule; LIPAM-14; neuroprotective; relaxant;
KW antithyroid; antidiabetic; cytostatic; dermatological; immunosuppressive;
KW antiinflammatory; thymimetic; antiallergic; cerebroprotective;
KW gastrointestinal; hepatotropic; nephrotropic; anticonvulsant;
KW antiparkinsonian; antibacterial; antiparasitic; fungicide; protozoacide;
KW virucide; uropathic; antirheumatic; cardiant; cardiovascular; anti-HIV;
KW nootropic.
XX
OS Homo sapiens.
XX
PN WO2003083081-A2.
XX
XX 09-OCT-2003.
XX
PF 27-MAR-2003; 2003WO-US009755.
XX
XX 29-MAR-2002; 2002US-0368722P.
PR 03-MAY-2002; 2002US-0377576P.
PR 05-JUL-2002; 2002US-0393934P.
PR 27-SEP-2002; 2002US-0414269P.
XX
XX (INCY-) INCYTE CORP.
XX
PI Emerling BM, Marquis JP, Chawla NK, Lee SY, Duggan BM, Warren BA;
PI Baughn MR, Lee EA, Griffin JA, Kable AE, Elliott VS, Chang H;
PI Lee S, Ramkumar J, Bulloch SA, Hafalia AJA, Khare R, Jiang X;
PI Jackson AA;
XX
DR WPI; 2003-788347/74.
DR N-PSDB; ADD93426.
XX
PT New LIPAM polypeptides, useful for diagnosing, preventing, and treating
PT disorders associated with abnormal expression or activity of LIPAM, e.g.
PT neuromuscular, immunological, cardiovascular disorders, cancer and/or
PT infections.
XX
PS Claim 69; Page 206-207; 238pp; English.
XX
CC The present sequence is the protein sequence of human lipid-associated
CC molecule LIPAM-14 (Incyte polypeptide 751262CD1), a protein that shows
CC homology to human Ca2+-independent phospholipase A2 short isoform. This
CC is one of 19 LIPAM polypeptides of the invention. The invention relates
CC to these novel LIPAMs and the nucleic acids encoding them, and to the use
CC of nucleic acids and proteins in the diagnosis, treatment and prevention
CC of disorders associated with abnormal expression or activity of LIPAM
CC such as neurodegenerative disorders (e.g. Parkinson's disease,
CC Alzheimer's disease), muscular disorders (e.g. myotonic dystrophy,
CC catatonica), endocrine disorders (e.g. diabetes, Grave's disease), cancers
CC (e.g. leukemia, cervical or breast cancers), immunological disorders
CC (e.g. scleroderma, systemic lupus erythematosus, allergies),
CC gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g.
CC Goodpasture's syndrome), infections (e.g. viral, bacterial, fungal,
CC parasitic, protozoal, helminthic), cardiovascular disorders (e.g.

inflammation; inhibitor; antiinflammatory.

Homo sapiens.

WO9717448-A2.

15-MAY-1997.

07-NOV-1996; 96WO-US017794.

08-NOV-1995; 95US-00555568.

(GENY) GENETICS INST INC.

Jones S, Tang J;

WPI; 1997-281037/25.

N-PSDB; AAT68826.

Calcium independent phospholipase A2/B - used to reduce inflammation in a mammalian subject.

Claim 12; Page 54-56; 74pp; English.

A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17848) is characterized by activity in the absence of calcium, by activity in a mixed micelle assay with 1-palmitoyl-2-(14C) - arachidonyl-phosphatidylcholine of about 1-20 $\mu\text{mol}/\text{min}\cdot\text{mg}$, by a pH optimum of 6, a lack of stimulation by ATP, and by including in its sequence at least one of the amino acid sequences given in AAW17839-44). It is an alternatively spliced variant of another isolated polypeptide (AAW17846) and is encoded by an isolated cDNA (AAT68826). Other PLA2/B enzymes (AAW17845, AAW17847) have also been identified. sPLA2/B enzymes are thought to be involved in the release of arachidonic acid in specific tissues. Recombinant sPLA2/B polypeptides produced in transformed host cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory drugs which inhibit the arachidonic acid cascade

Sequence 688 AA;

Query Match 100.0%; Score 1531; DB 2; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LQDLMHISRARKPAFIFLGSMDRDEKTHDHLCLDGGGVKGLIIQLIIAIEKASGVATKD 60
397 LQDLMHISRARKPAFIFLGSMDRDEKTHDHLCLDGGGVKGLIIQLIIAIEKASGVATKD 456

61 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEFLKREFGE 120
457 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEFLKREFGE 516

121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180
517 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 576

181 WRAARSSGAAPTYFRPNRFLDGLGLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240
577 WRAARSSGAAPTYFRPNRFLDGLGLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 636

241 VSLGTRSPQVPVTCVDVFRPNPNWELAKTVFGAKELGMVVDCCDTPDGRP 292
637 VSLGTRSPQVPVTCVDVFRPNPNWELAKTVFGAKELGMVVDCCDTPDGRP 688

RESULT 6
ABH82232
ID ABH82232 standard; protein; 688 AA.
XX
AC ABH82232;
XX
DT 08-JAN-2003 (first entry)
XX

Human cPLA2/B splice variant (clone 19b).

Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme; antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic; antiasthmatic; human.

Homo sapiens.

US2002106364-A1.

08-AUG-2002.

09-AUG-2001; 2001US-00927180.

27-JUL-1994; 94US-00281193.

14-APR-1995; 95US-00422106.

14-APR-1995; 95US-00422420.

26-JUN-1995; 95WO-US008069.

08-NOV-1995; 95US-00555568.

09-SEP-1998; 98US-00149988.

06-MAR-2000; 2000US-00519223.

(GENY) GENETICS INST INC.

Jones S, Tang J;

WPI; 2002-739923/80.

N-PSDB; ABV73011.

Novel composition comprising purified mammalian calcium independent phospholipase enzyme, useful for the screening of inhibitors of phospholipase activity, is active in the absence of calcium.

Claim 6; Page 28-30; 41pp; English.

The invention relates to a purified mammalian calcium independent cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is characterized by activity in the absence of calcium and has a molecular weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified calcium independent phospholipase enzyme is useful for identifying an inhibitor of phospholipase activity which involves combining (I), phospholipid and candidate inhibitor compound, and observing whether the enzyme cleaves the phospholipid and releases fatty acid from it. A pharmaceutical composition (PC) comprising a therapeutically effective amount of the inhibitor is useful for reducing inflammation and for treating inflammatory conditions including rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease and other diseases mediated by increased levels of prostaglandins, leukotriene or platelet activating factor. A composition comprising an antibody which binds to (I) is useful as research and diagnostic tool, and is also useful in the study of phospholipase A2 activity and inflammatory conditions. The present sequence represents a human cPLA2/B enzyme longer splice variant (clone 19b)

Sequence 688 AA;

Query Match 100.0%; Score 1531; DB 5; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LQDLMHISRARKPAFIFLGSMDRDEKTHDHLCLDGGGVKGLIIQLIIAIEKASGVATKD 60
397 LQDLMHISRARKPAFIFLGSMDRDEKTHDHLCLDGGGVKGLIIQLIIAIEKASGVATKD 456

61 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEFLKREFGE 120
457 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEFLKREFGE 516

121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180
517 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 576

181 WRAARSSGAAPTYFRPNRFLDGLGLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240

PT Calcium independent phospholipase A2/B - used to reduce inflammation in a
XX mammalian subject.
PS Claim 12; Page 49-51; 74pp; English.
XX
XX A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17847) is
CC characterized by activity in the absence of calcium, by activity in a
CC mixed micelle assay with 1-palmitoyl-2-(14C) - arachidonyl-
CC phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a
CC lack of stimulation by ATP, and by including in its sequence at least one
CC of the amino acid sequences given in AAW17839- 44). It is an
CC alternatively spliced variant of another isolated polypeptide (AAW17845)
CC and is encoded by an isolated cDNA (AAW68825). Other PLA2/B enzymes
CC (AAW17846, AAW17848) have also been identified. sPLA2/B enzymes are
CC thought to be involved in the release of arachidonic acid in specific
CC tissues. Recombinant sPLA2/B polypeptides produced in transformed host
CC cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory
CC drugs which inhibit the arachidonic acid cascade
XX
SQ Sequence 687 AA;
Query Match 100.0%; Score 1531; DB 2; Length 687;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQDLMHISRARKPAFLTSGMRDEKTRTHLLCLDGGGVKGLIIIIQLLIAIEKASGVATKD 60
DB 396 LQDLMHISRARKPAFLTSGMRDEKTRTHLLCLDGGGVKGLIIIIQLLIAIEKASGVATKD 455
QY 61 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVRGSRPYESGPLEFLKREFGE 120
DB 456 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVRGSRPYESGPLEFLKREFGE 515
QY 121 HTKMTDVRKPKVMTGTLSDROPAPAEHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180
DB 516 HTKMTDVRKPKVMTGTLSDROPAPAEHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 575
QY 181 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIV 240
DB 576 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIV 635
QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPPGRP 292
DB 636 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPPGRP 687
RESULT 4
ABB82231
XX ABB82231 standard; protein; 687 AA.
XX
XX ABB82231;
XX
XX
DT 08-JAN-2003 (first entry)
XX
DE Human cPLA2/B splice variant (clone 19a).
DE
DE
KW Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
KW antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;
KW antiasthmatic; human.
XX
XX Homo sapiens.
XX
XX US2002106364-A1.
XX
XX 08-AUG-2002.
XX
XX 09-AUG-2001; 2001US-00927180.
XX
XX 27-JUL-1994; 94US-00281193.
PR 14-APR-1995; 95US-00422106.
PR 14-APR-1995; 95US-00422420.
PR 26-JUN-1995; 95WO-US008069.
PR 08-NOV-1995; 95US-00555568.

PR 09-SEP-1998; 98US-00149988.
PR 06-MAR-2000; 2000US-00519223.
XX (GEMY) GENETICS INST INC.
PA Jones S, Tang J;
XX
PI
XX WPI; 2002-739923/80.
DR N-PSDB; ABV73010.
XX
XX Novel composition comprising purified mammalian calcium independent
PT phospholipase enzyme, useful for the screening of inhibitors of
PT phospholipase activity, is active in the absence of calcium.
XX
XX Claim 6; Page 23-25; 41pp; English.
XX
CC The invention relates to a purified mammalian calcium independent
CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
CC characterized by activity in the absence of calcium and has a molecular
CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
CC calcium independent phospholipase enzyme is useful for identifying an
CC inhibitor of phospholipase activity which involves combining (I),
CC phospholipid and candidate inhibitor compound, and observing whether the
CC enzyme cleaves the phospholipid and releases fatty acid from it. A
CC pharmaceutical composition (PC) comprising a therapeutically effective
CC amount of the inhibitor is useful for reducing inflammation and for
CC treating inflammatory conditions including rheumatoid arthritis,
CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
CC by increased levels of prostaglandins, leukotriene or platelet activating
CC factor. A composition comprising an antibody which binds to (I) is useful
CC as research and diagnostic tool, and is also useful in the study of
CC phospholipase A2 activity and inflammatory conditions. The present
CC sequence represents a human cPLA2/B enzyme longer splice variant (clone
CC 19a)
XX
SQ Sequence 687 AA;
Query Match 100.0%; Score 1531; DB 5; Length 687;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQDLMHISRARKPAFLTSGMRDEKTRTHLLCLDGGGVKGLIIIIQLLIAIEKASGVATKD 60
DB 396 LQDLMHISRARKPAFLTSGMRDEKTRTHLLCLDGGGVKGLIIIIQLLIAIEKASGVATKD 455
QY 61 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVRGSRPYESGPLEFLKREFGE 120
DB 456 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVRGSRPYESGPLEFLKREFGE 515
QY 121 HTKMTDVRKPKVMTGTLSDROPAPAEHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180
DB 516 HTKMTDVRKPKVMTGTLSDROPAPAEHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 575
QY 181 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIV 240
DB 576 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIV 635
QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPPGRP 292
DB 636 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPPGRP 687
RESULT 5
AAW17848
ID AAW17848 standard; protein; 688 AA.
XX
XX AAW17848;
XX
XX 07-AUG-1997 (first entry)
DT
XX Cytosolic phospholipase A2/B (alternatively spliced clone 19b).
DE
XX Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
KW

XX	Sequence 292 AA;	CC	Characterized by activity in the absence of calcium and has a molecular weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified calcium independent phospholipase enzyme is useful for identifying an inhibitor of phospholipase activity which involves combining (I), phospholipid and candidate inhibitor compound, and observing whether the enzyme cleaves the phospholipid and releases fatty acid from it. A pharmaceutical composition (PC) comprising a therapeutically effective amount of the inhibitor is useful for reducing inflammation and for treating inflammatory conditions including rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease and other diseases mediated by increased levels of prostaglandins, leukotriene or platelet activating factor. A composition comprising an antibody which binds to (I) is useful as research and diagnostic tool, and is also useful in the study of phospholipase A2 activity and inflammatory conditions. The present sequence represents a human cPLA2/B enzyme (clone 19b)
SQ		XX	
Query Match	100.0%; Score 1531; DB 5; Length 292;		
Best Local Similarity	100.0%; Pred. No. 2.9e-163;		
Matches 292; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 LQDLMHISARKAPAFILGSMRDEKTHDHLCLDGGGVKGLIIQLIIAIEKASGVATKD 60	QY	1 LQDLMHISARKAPAFILGSMRDEKTHDHLCLDGGGVKGLIIQLIIAIEKASGVATKD 60
DB	1 LQDLMHISARKAPAFILGSMRDEKTHDHLCLDGGGVKGLIIQLIIAIEKASGVATKD 60	DB	1 LQDLMHISARKAPAFILGSMRDEKTHDHLCLDGGGVKGLIIQLIIAIEKASGVATKD 60
QY	61 LFDWVAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEFLKREFGE 120	QY	61 LFDWVAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEFLKREFGE 120
DB	61 LFDWVAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEFLKREFGE 120	DB	61 LFDWVAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEFLKREFGE 120
QY	121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180	QY	121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180
DB	121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180	DB	121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180
QY	181 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240	QY	181 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240
DB	181 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240	DB	181 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240
QY	241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVVDCTDPPDGRP 292	QY	241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVVDCTDPPDGRP 292
DB	241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVVDCTDPPDGRP 292	DB	241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVVDCTDPPDGRP 292
RESULT 3			
AAW17847		AAW17847	
ID	AAW17847 standard; protein; 687 AA.	ID	AAW17847 standard; protein; 687 AA.
XX		XX	
AC	AAW17847;	AC	AAW17847;
XX		XX	
DT	07-AUG-1997 (first entry)	DT	07-AUG-1997 (first entry)
XX		XX	
DE	Cytosolic phospholipase A2/B (alternatively spliced clone 19a).	DE	Cytosolic phospholipase A2/B (alternatively spliced clone 19a).
XX		XX	
KW	Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade; inflammation; inhibitor; antiinflammatory.	KW	Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade; inflammation; inhibitor; antiinflammatory.
XX		XX	
OS	Homo sapiens.	OS	Homo sapiens.
XX		XX	
PN	WO9717448-A2.	PN	WO9717448-A2.
XX		XX	
PD	15-MAY-1997.	PD	15-MAY-1997.
XX		XX	
PF	07-NOV-1996; 96WO-US017794.	PF	07-NOV-1996; 96WO-US017794.
XX		XX	
PR	08-NOV-1995; 95US-00555568.	PR	08-NOV-1995; 95US-00555568.
XX		XX	
PA	(GEMY) GENETICS INST INC.	PA	(GEMY) GENETICS INST INC.
XX		XX	
PI	Jones S, Tang J;	PI	Jones S, Tang J;
XX		XX	
DR	WPI; 1997-281037/25.	DR	WPI; 1997-281037/25.
XX		XX	
DR	N-PSDB; AAT68825.	DR	N-PSDB; AAT68825.
XX		XX	

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:05:39 ; Search time 37.6866 Seconds
(without alignments)
2996.666 Million cell updates/sec

Title: US-10-612-668-19
Perfect score: 1531
Sequence: 1 LQDLMHISRAKPAFILGSM.....GAKELGKMVVDCTDPDGRP 292

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: genesecp1980s:*
- 2: genesecp1990s:*
- 3: genesecp2000s:*
- 4: genesecp2001s:*
- 5: genesecp2002s:*
- 6: genesecp2003as:*
- 7: genesecp2003bs:*
- 8: genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1531	100.0	292	2	AAW17846	Cytosolic
2	1531	100.0	292	5	ABB82230	Calcium i
3	1531	100.0	687	2	AAW17847	Cytosolic
4	1531	100.0	687	5	ABB82231	Human cpl
5	1531	100.0	688	2	AAW17848	Cytosolic
6	1531	100.0	688	5	ABB82232	Human cpl
7	1524	99.5	667	7	ADM05093	Human pro
8	1524	99.5	784	7	ADQ93407	Human lip
9	1524	99.5	806	5	AAE25968	Human PLA
10	1524	99.5	806	8	ADQ19776	Human pro
11	1499	97.9	810	8	ABM84355	Human dia
12	1499	97.9	810	8	ABM84354	Human dia
13	1471	96.1	752	2	AAR83018	Calcium-i
14	1471	96.1	752	2	AAW01479	Calcium-i
15	1471	96.1	752	2	AAW13163	Ca-indepe
16	1471	96.1	752	2	AAW17849	Hamster c
17	1471	96.1	752	2	AAW81825	Chinese h
18	1471	96.1	752	5	ABB82215	Calcium i
19	1454	95.0	751	7	ADG46244	Rat Prote
20	1454	95.0	751	7	ADE60532	Rat Prote
21	1454	95.0	751	7	ADE55230	Rat Prote
22	1454	95.0	751	7	ADE60536	Rat Prote
23	890	58.1	401	4	AAW82811	Human pro
24	736	48.1	877	4	ABB62624	Drosophil
25	456.5	29.8	1071	8	ADN24212	Bacterial

ALIGNMENTS

RESULT 1

AAW17846
ID AAW17846 standard; protein; 292 AA.

XX
AC AAW17846;

XX
DT 07-AUG-1997 (first entry)

XX
DE Cytosolic phospholipase A2/B (clone 19b product) .

XX
XX Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;

KW Inflammation; inhibitor; antiinflammatory.

XX
OS Homo sapiens.

XX
PN WO9717448-A2.

XX
PD 15-MAY-1997.

PF 07-NOV-1996; 96WO-US017794 .

PR 08-NOV-1995; 95US-00555568.

XX
(GEMY) GENETICS INST INC.

XX
Jones S, Tang J;

XX
WPI; 1997-281037/25.

XX
N-PSDB; AAT68824.

PT Calcium independent phospholipase A2/B - used to reduce inflammation in a mammalian subject.

XX
Claim 12; Page 46-47; 74pp; English.

XX
A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17845) is characterised by activity in the absence of calcium, by activity in a mixed micelle assay with 1-palmitoyl-2-(14C)- arachidonyl-phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a lack of stimulation by ATP, and by including in its sequence at least one of the amino acid sequences given in AAW17839- 44). It is encoded by partial cDNA clone 19b (AAT68824), derived from Burkitt's lymphoma Raji (ATCC CRL86) cells. Other PLA2/B enzymes (AAW17845, AAW17847-48) have also been identified. sPLA2/B enzymes are thought to be involved in the release of arachidonic acid in specific tissues. Recombinant sPLA2/B polypeptides produced in transformed host cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory drugs which inhibit the arachidonic acid cascade

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Job time : 50.4624 secs

[illegible]

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Db          912 VD-PSVFEMNDLEGMLR---GMKNLSLVVIDQATATEGAP 947

Search completed: May 26, 2005, 14:19:30
Job time : 50.4624 secs

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smillus D.E., Schnerk A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC067375; AH67375.1; -.
DR HSSP; P20749; IKIB.
DR ZFIN; ZDB-GENE-040426-2079; zgc:77476.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKVRIN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR ANK repeat.
SQ SEQUENCE 818 AA; 90691 MW; C7B5CD45401F8EA9 CRC64;

Query Match 63.1%; Score 966.5; DB 2; Length 818;
Best Local Similarity 63.9%; Pred. No. 4.4e-78;
Matches 184; Conservative 31; Mismatches 48; Indels 25; Gaps 1;

QY 28 DHLCLDGGVKGGLIIQLIIAIEKASGVATKDLFDWVAGTSGGILALAILHLSKSMAY 87
DB 465 DRLLCLDGGIGKGLVLIQLIIAIEKEAGRIPLRFLFDVSVSTGGILALIVHGSWEYL 524

QY 88 RGMFYFMKDEVFGRSPYSGPLEEFKREFGHTKMTDVRPKVMLTGTLSDRQPAELH 147
DB 525 RCLYFRMKQVFKGSRPYSGPLEEFKNEFGENTKMTDTPRVNMTSVLADRHFGELH 584

QY 148 LFRNYDAPETVREPRFNQNVNLRPPAQP-----SDQLVWR 182
DB 585 LFRNYDPPALQNDPPYKSTATQPLTVPGWEDEDLVGYTRPPKRRKRVTDSEQLVWR 644

QY 183 AARSSGAAPTYFRPNGRFLDGGLLANNPTLDAMTEIHEYNQDLIRKGQANKVKLSIVVS 242
DB 645 AARSSGAAPTYFRPMGRFLDGGLLANNPTLDAMTEIHFQFKALKAQGRDEVTRLGVVVS 704

QY 243 LGTGRSPQVPVTCVDVFRPSNPMELAKTVFGAKELGKMWVDCCTDPDG 290
DB 705 LGTGKPPQAVNSVDVFRPSNPIELAKTVFGVKELGKMLVDCCTDSGD 752

RESULT 9
Q8MR13 PRELIMINARY; PRT; 386 AA.
AC Q8MR13;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LD44515P.
GN ORFNames=CG6718;
OS Drosophila melanogaster (Fruit fly).
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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dreesek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Faragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV12192; NAM5704.1; -.
DR FlyBase; FBgn0036053; CG6718.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF01734; Patatin; 1.
SQ SEQUENCE 386 AA; 42693 MW; B32B7BCFC38541DD CRC64;

Query Match 48.1%; Score 736; DB 2; Length 386;
Best Local Similarity 50.9%; Pred. No. 1e-57;
Matches 142; Conservative 47; Mismatches 84; Indels 6; Gaps 2;

QY 16 ILGSMRDEKRTDHLCLDGGVKGGLIIQLIIAIEKASGVATKDLFDWVAGTSGGILA 75
DB 48 IAAFIGDKPYGRGLLCLDGGIGRLVQLVQMLEIEKLSRTPIIHPDWTAGTSGGILA 107

QY 76 LAILHSKSMAYMRGMVFRMKDVFGRSPYSGPLEEFKREFGHTKMTDVRKPKVMLT 135
DB 108 LALGCGKTKRQCMGLYLRMKEQCFVGRSPYSGPLEEFKILKDLNGEENWMTDIKPKIMVT 167

QY 136 GTLSDRQPAELHFRNYDAPETVR---EPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPT 192
DB 168 GVMADRKPDVHLFRNYTSASDILGIVTPIINNRI---PPQPSEQLVWRAARATGAAPS 224

QY 193 YFRPNGRFLDGGLLANNPTLDAMTEIHEYNQDLIRKGQANKVKLSIVVSLGTRSPQVP 252
DB 225 YFRAGRFLDGGLLANNPTLDAMTEIHEYNALRSAGRESEAIPIVSNVMSLGTGHIPVTE 284

QY 253 VTCVDVFRPSNPMELAKTVFGAKELGKMWVDCCTDPDGR 291
DB 285 LKXIDVFRPESWDTKLAYGISTIGNLVLDQATCSDGR 323

RESULT 10
Q9VT60 PRELIMINARY; PRT; 877 AA.
AC Q9VT60;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG6718-PA.
GN ORFNames=CG6718;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabo G.L.,
RA April J.F., Agbayani A., An H.J., Andrews-Frannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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DR Pfam; PF00023; Ank; 6.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS00297; ANK_REPEAT; 1.
KW ANK repeat; Hypothetical Protein.
SQ SEQUENCE 807 AA; 8955 MW; 1B9018AE1B2D252F CRC64;

Query Match 94.7%; Score 1450; DB 2; Length 807;
Best Local Similarity 93.8%; Pred. No. 1e-121; 8; Indels 0; Gaps 0;
Matches 273; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 LQDLMHISARKPAFILSGMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
DB 452 LQDLMPVSRARKPAFILSGMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 511
QY 61 LFDWVAGTGTGILALAILHSKSMAYMRGMVFRMKDEVERGSRPYESGPLEEFLKREFGE 120
DB 512 LFDWVAGTGTGILALAILHSKSMAYMRGMVFRMKDEVERGSRPYESGPLEEFLKREFGE 571
QY 121 HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQVNLRRPPAQPSDQLV 180
DB 572 HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQVNLRRPPAQPSDQLV 631
QY 181 WTAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240
DB 632 WTAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 691
QY 241 VSLGTGRSPQVPVTCVDFRPNPNWELAKTVFGAKELGKVVDCCTDPPGR 291
DB 692 VSLGTGRSPQVPVTCVDFRPNPNWELAKTVFGAKELGKVVDCCTDPPGR 742

RESULT 7
Q6DDKO PRELIMINARY; PRT; 756 AA.
ID Q6DDKO
AC Q6DDKO
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DE MGC83523 protein.
GN Name=MGC83523;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeb B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC077558; AAH77558.1; -;
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0045735; F: nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 7.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 7.
DR PROSITE; PS00088; ANK_REPEAT; 3.
DR PROSITE; PS00297; ANK_REPEAT; 1.
KW ANK repeat.
SQ SEQUENCE 756 AA; 84303 MW; C0278741CCA52A71 CRC64;

Query Match 68.1%; Score 1042; DB 2; Length 756;
Best Local Similarity 67.9%; Pred. No. 6.2e-85;
Matches 199; Conservative 34; Mismatches 56; Indels 4; Gaps 1;

QY 2 QDLMHISARK----PAFILSGMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVA 57
DB 398 RDFVYVSTALSGMLVPQDTVDFREDGLRVKDRLLCLDGGGIRGLVLMQLLIAIEKAGRP 457
QY 58 TKDLFDWVAGTGTGILALAILHSKSMAYMRGMVFRMKDEVERGSRPYESGPLEEFLKRE 117
DB 458 IRELFDWVSGTGTGILALAILHGMPMESVRCILFRMKNEVFGSRPYESGPLEEFLKKE 517
QY 118 FGEHTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQVNLRRPPAQPSD 177
DB 518 FGENTKMSDVNRNPKVIVTGLSDRHPAELHLFRNYDPEPDPETDHEPPYKSVASFRPVTTAE 577
QY 178 QLVWTAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKKL 237
DB 578 QLVWTAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNTCLKKGKMGAGQVKL 637
QY 238 STVSVSLGTGRSPQVPVTCVDFRPNPNWELAKTVFGAKELGKVVDCCTDPPG 290
DB 638 GIVSLGTGKPPQISVGSVDVFRPNPNWELAKTVFGAKELGKVVDCCTDSDG 690

RESULT 8
Q6NWO PRELIMINARY; PRT; 818 AA.
ID Q6NWO
AC Q6NWO
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE ZGC:77476.
GN ORFNames=zgc:77476;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeb B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeb B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLPFRNYDAPETVREPRNQNNVLRPPAQPDSQVLV 180
Db 572 HTKMTDVKKPKVMTGTLSDRQPAELHLPFRNYDAPAVREPRCNQNLKPPTQPADQLV 631
QY 181 WRAARSSGAAPTYFRPNRGFLDGLGGLANNPTLDAMTEIHEYNOIDLIRKQANKVKLSIV 240
Db 632 WRAARSSGAAPTYFRPNRGFLDGLGGLANNPTLDAMTEIHEYNOIDLIRKQANKVKLSIV 691
QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR 291
Db 692 VSLGTGKSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR 742

RESULT 5
PA26 RAT STANDARD; PRT; 751 AA.
AC P97570;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (CaI-PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=Pla2g6;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Pancreatic islets;
RX MEDLINE=97269008; PubMed=9111008; DOI=10.1074/jbc.272.17.11250;
RA Ma Z., Ramanadham S., Kempe K., Chi X.S., Ladenson J., Turk J.;
RT "Pancreatic islets express a Ca2+-independent phospholipase A2 enzyme that contains a repeated structural homologous to the integral membrane protein binding domain of ankyrin.";
RL J. Biol. Chem. 272:11118-11127(1997).
CC -!- FUNCTION: Catalyzes the release of fatty acids from phospholipids. It has been implicated in normal phospholipid remodeling, nitric oxide-induced or vasopressin-induced arachidonic acid release and in leukotriene and prostaglandin production. May participate in fas mediated apoptosis and in regulating transmembrane ion flux in glucose-stimulated B-cells.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a carboxylate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Found in brain, lung, spleen, kidney, liver, heart and skeletal muscle.
CC -!- SIMILARITY: Contains 7 ANK repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U51898; AAC53136.1; -.
DR HSSP; Q60778; IOY3.
DR RGD; 628867; Pla2g6.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; Ank; 6.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS50088; ANK REPEAT; 4.
DR PROSITE; PS50297; ANK REP REGION; 1.
KW ANK repeat; Hydrolase; Lipid degradation; Repeat.
FT REPEAT 150 180 ANK 1.
FT REPEAT 184 214 ANK 2.
FT REPEAT 218 247 ANK 3.
FT REPEAT 250 280 ANK 4.
FT REPEAT 285 311 ANK 5.
FT REPEAT 315 344 ANK 6.
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FT REPEAT 348 377 ANK 7.
FT ACT_SITE 464 464 Potential.
SQ SEQUENCE 751 AA; 83582 MW; 393BBBADA7FCC99B CRC64;

Query Match 95.0%; Score 1454; DB 1; Length 751;
Best Local Similarity 94.2%; Pred. NO. 4.1e-122;
Matches 274; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 LQDLMHISRRAPKPAFTLGSMDKRTKTHDHLCLDGGGVKGLIIQLIIAIEKASGVATKD 60
Db 396 LQDLMPVSRAPKPAFTLSSMDKRTKTHDHLCLDGGGVKGLVIIQLIIAIEKASGVATKD 455
QY 61 LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFGRSGPYESGPLEEFLKREFGE 120
Db 456 LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFGRSGPYESGPLEEFLKREFGE 515
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLPFRNYDAPETVREPRNQNNVLRPPAQPDSQVLV 180
Db 516 HTKMTDVKKPKVMTGTLSDRQPAELHLPFRNYDAPAVREPRCNQNLKPPTQPADQLV 575
QY 181 WRAARSSGAAPTYFRPNRGFLDGLGGLANNPTLDAMTEIHEYNOIDLIRKQANKVKLSIV 240
Db 576 WRAARSSGAAPTYFRPNRGFLDGLGGLANNPTLDAMTEIHEYNOIDLIRKQANKVKLSIV 635
QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR 291
Db 636 VSLGTGKSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR 686

RESULT 6
Q66HD1 PRELIMINARY; PRT; 807 AA.
AC Q66HD1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.P., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Smaluk U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC081916; AAH81916.1; -.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RX STRAIN=C3H/He; TISSUE=Osteoblast;
RA STRAIN=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He; TISSUE=Osteoblast;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052845; AAH52845.1; -.
DR HSSP; P07207; 1078.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF01734; Patatin; 1.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat.
SQ SEQUENCE 752 AA; 83717 MW; DAC3347B0E14AAFC CRC64;

Query Match
Best Local Similarity 94.8%; Score 1463; DB 2; Length 752;
Matches 276; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 LODLHMSIRKPAFILSGMRDEKTHDHLCLDGGVKGGLIIQLLIAEKASGVATKD 60
DB 397 LODLHMSIRKPAFILSGMRDEKTHDHLCLDGGVKGGLIIQLLIAEKASGVATKD 456
QY 61 LFDWAGTGTGGLALAILHKSMAVMGMVFRMKDEVFRGSRPYESGPLEFLKREFGE 120
DB 457 LFDWAGTGTGGLALAILHKSMAVMGMVFRMKDEVFRGSRPYESGPLEFLKREFGE 516
QY 121 HTKMTDVRKPKVMTLTSLDRPDAELHLPFRNYDAPETVREPRNQNVNLRPPAQPSDQIV 180
DB 517 HTKMTDVRKPKVMTLTSLDRPDAELHLPFRNYDAPETVREPRNQNVNLRPPAQPSDQIV 576
QY 181 WRAARSSGAAPTYFRPNRFLDGLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240
DB 577 WRAARSSGAAPTYFRPNRFLDGLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 636
QY 241 VSLGTGRSPQVPTCVDFRPNPNWELAKTVFGAKELGKQVDCCTDPDGR 291
DB 637 VSLGTGRSPQVPTCVDFRPNPNWELAKTVFGAKELGKQVDCCTDPDGR 687

RESULT 4
Q9UK61

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ID Q9UK61 PRELIMINARY; PRT; 807 AA.
AC Q9UK61;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ca2+-independent phospholipase A2 long form (Pla2g6 protein).
GN Name=Pla2g6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIH/Swiss;
RA Chiu C.-H., Jackowski S.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF259401; AAF72651.1; -.
DR EMBL; BC057209; AAH57209.1; -.
DR HSSP; Q60778; 10Y3.
DR MGD; MGI:1859152; Pla2g6.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat.
SQ SEQUENCE 807 AA; 89559 MW; 3838889731100294 CRC64;

Query Match
Best Local Similarity 95.6%; Score 1463; DB 2; Length 807;
Matches 276; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 LODLHMSIRKPAFILSGMRDEKTHDHLCLDGGVKGGLIIQLLIAEKASGVATKD 60
DB 452 LODLHMSIRKPAFILSGMRDEKTHDHLCLDGGVKGGLIIQLLIAEKASGVATKD 511
QY 61 LFDWAGTGTGGLALAILHKSMAVMGMVFRMKDEVFRGSRPYESGPLEFLKREFGE 120
DB 512 LFDWAGTGTGGLALAILHKSMAVMGMVFRMKDEVFRGSRPYESGPLEFLKREFGE 571

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RN SEQUENCE FROM N.A.
 RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
 RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
 RA Clump M., Smith L.J., Alnough R., Almeida J.P., Babbage A.K.,
 RA Baguley C., Bailey J., Barlow K.P., Bates K.N., Beasley O.P.,
 RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
 RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
 RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
 RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
 RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
 RA Hunt S.B., Jones M.C., Kershaw J., Kimberley A.M., King A.,
 RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
 RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T.,
 RA McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
 RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
 RA Vaubin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudon J.,
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
 RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
 RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
 RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
 RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
 RA Wilson R., Emanuel B.S., Shaikh T., Kuranashi H., Saitta S.,
 RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
 RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
 RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
 RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
 RA Khan A.S., Lane L., Tilahun Y., Wright H.;
 RT "The DNA sequence of human chromosome 22.";
 RL Nature 402:489-495(1999).
 [7]
 RN SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2).
 RC TISSUE=Brain;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uddin T.B., Tetsuyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Catalyzes the release of fatty acids from phospholipids.
 CC It has been implicated in normal phospholipid remodelling, nitric
 CC oxide-induced or vasopressin-induced arachidonic acid release and

CC in leukotriene and prostaglandin production. May participate in
 CC fas mediated apoptosis and in regulating transmembrane ion flux in
 CC glucose-stimulated B-cells.
 CC -!- FUNCTION: Isoform ankyrin-iPLA2-1 and isoform ankyrin-iPLA2-2,
 CC which lack the catalytic domain, are probably involved in the
 CC negative regulation of iPLA2 activity.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a carboxylate.
 CC -!- SUBUNIT: Forms large oligomeric 270-350 kDa structures.
 CC -!- SUBCELLULAR LOCATION: Isoform LH-IPLA2 was found to be membrane
 CC bound. Isoform SH-IPLA2 is cytoplasmic.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=LH-IPLA2; IsoId=O60733-1; Sequence=Displayed;
 CC Name=SH-IPLA2;
 CC IsoId=O60733-2; Sequence=VSP_000278;
 CC Name=Ankyrin-iPLA2-1;
 CC IsoId=O60733-3; Sequence=VSP_000281, VSP_000282;
 CC Name=Ankyrin-iPLA2-2;
 CC IsoId=O60733-4; Sequence=VSP_000277, VSP_000279, VSP_000280;
 CC -!- TISSUE SPECIFICITY: Four different transcripts were found to be
 CC expressed in a distinct tissue distribution.
 CC -!- SIMILARITY: Contains 7 ANK repeats.

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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 CC EMBL; AF064594; AAC37486.1; -
 CC EMBL; AF102988; AAD41722.1; -
 CC EMBL; AF102989; AAD41723.1; -
 CC EMBL; AF117692; AAD30424.1; -
 CC EMBL; AF117697; AAD30424.1; JOINED.
 CC EMBL; AF117678; AAD30424.1; JOINED.
 CC EMBL; AF117679; AAD30424.1; JOINED.
 CC EMBL; AF117680; AAD30424.1; JOINED.
 CC EMBL; AF117681; AAD30424.1; JOINED.
 CC EMBL; AF117682; AAD30424.1; JOINED.
 CC EMBL; AF117683; AAD30424.1; JOINED.
 CC EMBL; AF117684; AAD30424.1; JOINED.
 CC EMBL; AF117685; AAD30424.1; JOINED.
 CC EMBL; AF117686; AAD30424.1; JOINED.
 CC EMBL; AF117687; AAD30424.1; JOINED.
 CC EMBL; AF117688; AAD30424.1; JOINED.
 CC EMBL; AF117689; AAD30424.1; JOINED.
 CC EMBL; AF117690; AAD30424.1; JOINED.
 CC EMBL; AF117691; AAD30424.1; JOINED.
 CC EMBL; AF116267; AAF34728.1; -
 CC EMBL; AF116253; AAF34728.1; JOINED.
 CC EMBL; AF116253; AAF34728.1; JOINED.
 CC EMBL; AF116254; AAF34728.1; JOINED.
 CC EMBL; AF116255; AAF34728.1; JOINED.
 CC EMBL; AF116256; AAF34728.1; JOINED.
 CC EMBL; AF116257; AAF34728.1; JOINED.
 CC EMBL; AF116258; AAF34728.1; JOINED.
 CC EMBL; AF116259; AAF34728.1; JOINED.
 CC EMBL; AF116260; AAF34728.1; JOINED.
 CC EMBL; AF116261; AAF34728.1; JOINED.
 CC EMBL; AF116262; AAF34728.1; JOINED.
 CC EMBL; AF116263; AAF34728.1; JOINED.
 CC EMBL; AF116264; AAF34728.1; JOINED.
 CC EMBL; AF116265; AAF34728.1; JOINED.
 CC EMBL; AF116266; AAF34728.1; JOINED.
 CC EMBL; AL080187; CAB45768.1; -
 CC EMBL; AY522921; AAR92478.1; -
 CC EMBL; AL022322; CAA18446.1; -
 CC EMBL; BC036742; AAH36742.2; -
 CC EMBL; BC051904; AAH51904.1; -

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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:06:44 ; Search time 47.4624 Seconds
(without alignments)
3150.433 Million cell updates/sec

Title: US-10-612-668-19

Perfect score: 1531

Sequence: 1 LQDLHISRARKPAFLGSM.....GAKELGKVVVDCCTDPDGRP 292

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1524	99.5	806	1	PA26 HUMAN	O60733 homo sapien
2	1463	95.6	752	1	PA26 MOUSE	P97819 mus musculu
3	1463	95.6	752	2	Q7TFX2	Q7tpx2 mus musculu
4	1463	95.6	807	2	Q9JRK61	Q9jrk61 mus musculu
5	1454	95.0	751	1	PA26 RAT	P97570 rattus norv
6	1450	94.7	807	2	Q66HD1	O66hd1 rattus norv
7	1042	68.1	756	2	Q6DDK0	O6ddk0 xenopus lae
8	966.5	63.1	818	2	Q6NMY0	O6nmy0 brachydanio
9	736	48.1	386	2	Q8MR13	Q8mr13 drosophila
10	736	48.1	877	2	Q9VT60	Q9vt60 drosophila
11	736	48.1	887	2	Q7KUD4	Q7kud4 drosophila
12	720	47.0	879	2	Q7Q2U1	Q7q2u1 anopheles g
13	456.5	29.8	1071	2	Q20500	Q20500 caenorhabdi
14	419	27.4	1021	2	Q810Q6	Q810q6 caenorhabdi
15	419	27.4	1023	2	Q62398	O62398 caenorhabdi
16	376	24.6	762	2	Q95YD2	Q95yd2 caenorhabdi
17	287	18.7	501	2	Q9N5L3	Q9n5l3 caenorhabdi
18	270.5	17.7	525	2	Q9TVS0	Q9tvs0 caenorhabdi
19	266	17.4	546	2	Q8MXR3	Q8mxr3 caenorhabdi
20	260	17.0	433	2	Q7Q158	Q7q158 anopheles g
21	255	16.7	1285	2	Q80693	Q80693 arabidopsis
22	253.5	16.6	456	2	Q22152	Q22152 caenorhabdi
23	235.5	15.4	355	2	Q9KYG8	Q9kyg8 vibrio chol
24	230.5	15.1	552	2	Q6JBI3	O6jbi3 dictyocaulu
25	230	15.0	459	2	Q6JBI2	O6jbi2 dictyocaulu
26	222	14.5	361	2	Q6XGD7	O6xgd7 escherichia
27	213.5	13.9	679	2	Q96176	Q96176 plasmodium
28	211.5	13.8	380	2	Q95035	Q95035 homo sapien
29	211.5	13.8	639	2	Q9H7T5	Q9h7t5 homo sapien
30	211.5	13.8	782	2	Q9NPF0	Q9npf0 homo sapien
31	210.5	13.7	776	2	Q8K1N1	Q8kin1 mus musculu

32	210.5	13.7	803	2	Q9DC20	O9dc20 mus musculu
33	204.5	13.4	577	2	Q9K5M3	Q9k5m3 anabaena ci
34	201	13.1	382	2	Q9M1W9	Q9m1w9 arabidopsis
35	201	13.1	384	2	Q93ZQ3	Q93zq3 arabidopsis
36	199.5	13.0	671	2	Q7RKE1	Q7rke1 plasmodium
37	198	12.9	390	2	Q8YUN7	Q8yun7 anabaena sp
38	193.5	12.6	387	2	Q671Z1	O671z1 oryza sativ
39	191	12.5	332	2	Q62AP1	O62ap1 burkholderi
40	191	12.5	332	2	Q63JR4	O63jr4 burkholderi
41	190.5	12.4	1294	2	Q7SFP66	Q7sf66 neospora
42	188	12.3	322	2	Q7POX4	Q7pox4 chromobacte
43	188	12.3	1409	2	Q69VY8	O69vy8 oryza sativ
44	187	12.2	302	2	Q73HJ4	Q73hj4 wolbachia p
45	185.5	12.1	401	2	Q9FIY1	O9fiy1 arabidopsis

ALIGNMENTS

RESULT 1
PA26_HUMAN STANDARD; PRT; 806 AA.
AC O60733; Q75645; Q8N452; Q9UG29; Q9UIT0; Q9Y671;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (iPLA2) (Cal-PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=PLA2G6; Synonym=IPLA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2; ANKYRIN-IPLA2-1 AND ANKYRIN-IPLA2-2).
RC TISSUE=B-cell, and Testis;
RX MEDLINE=98079046; PubMed=9417066; DOI=10.1074/jbc.273.1.207;
RA Larsson P.K.A., Claesson H.-E., Kennedy B.P.;
RT "Multiple splice variants of the human calcium-independent phospholipase A2 and their effect on enzyme activity.";
RL J. Biol. Chem. 273:207-214(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2).
RC TISSUE=Pancreatic islets;
RX MEDLINE=99194813; PubMed=10092647; DOI=10.1074/jbc.274.14.9607;
RA Ma Z., Wang X., Nowatzke W., Ramanadham S., Turk J.;
RT "Human pancreatic islets express mRNA species encoding two distinct catalytically active isoforms of group VI phospholipase A2 (iPLA2) that arise from an exon-skipping mechanism of alternative splicing of the transcript from the iPLA2 gene on chromosome 22q13.1.";
RL J. Biol. Chem. 274:9607-9616(1999).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=99269033; PubMed=10336645;
RA Larsson Forsell P.K.A., Kennedy B.P., Claesson H.-E.;
RT "The human calcium-independent phospholipase A2 gene. Multiple enzymes with distinct properties from a single gene.";
RL Eur. J. Biochem. 262:575-585(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM LH-IPLA).
RC TISSUE=Testis;
RX Ansoorge W., Winkner U., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS ILE-58; GLY-63; GLN-70; ASN-183 AND THR-343.
RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Sherwood A.M., Leithausen B.J., Nickerson D.A.;
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

```

Db      17 ILSLDGGVGRGIIAGVILAFLEKQLQELDGEARLADYFDVIAGTGTGGLVTAMLTVPDE 76
QY      84 MAYMRGMVFRMKDEYFRGSRPYE-----SGP-----LEE 112
Db      77 TG---RPHPAAKDIV-----PFYLEHCPKIFPQPTGVALLPKLLSGPKYSGKYLRLN 128
QY     113 FLKREFGE---HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNL 169
Db     129 LLSKLLGETRLHQTLTNI-----VPTFDIKKLOPT---IFSSY---QLLVDPSSLVKV-- 176
QY     170 RPPAQPSDQVWRAARSSGAAPTYFRPN-----GRFLDGGLLANNPTLDAMT 216
Db     177 -----SDICI-----GTSAAITFPFPHYFSNEDSQGNKTEFNLDGAVTANNPTLVAMT 225
QY     217 -----EIHEYNOQLIRKQANKVKLS-----IVVSLGTG 246
Db     226 AVSKQIVKKNPDM-----GKLPGLGDFRFLVISIGTG 257

RESULT 15
H85437
patatin-like protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H85437
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
  Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: H85437
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-414 <STO>
A:Cross-references: UNIPROT:O23179; GB:NC_001268; NID:g7270656; PIDN:CAB80373.1; GSPDB:G
C:Genetics:
A:Gene: AT4g37070
A:Map position: 4
C:Superfamily: patatin

Query Match      11.5%; Score 176; DB 2; Length 414;
Best Local Similarity 26.6%; Pred. No. 5.5e-08;
Matches 74; Conservative 36; Mismatches 70; Indels 98; Gaps 15;

QY     30 LCLDGGGVKGLIIQLLIAIEK-----ASGVATKDLFDWVAGTGTGILALAILHSHKS 83
Db     21 ILSLDGGVGRGIIAGVILAFLEKQLQELDGEARLADYFDVIAGTGTGGLVTAMLTVPDE 80
QY     84 MAYMRGMVFRMKDEYFRGSRPYE-----SGP-----LEE 112
Db     81 TG---RPHPAAKDIV-----PFYLEHCPKIFPQPTGVALLPKLLSGPKYSGKYLRLN 132
QY     113 FLKREFGE---HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNL 169
Db     133 LLSKLLGETRLHQTLTNI-----VPTFDIKKLOPT---IFSSY---QLLVDPSSLVKV-- 180
QY     170 RPPAQPSDQVWRAARSSGAAPTYFRPN-----GRFLDGGLLANNPTLDAMT 216
Db     181 -----SDICI-----GTSAAITFPFPHYFSNEDSQGNKTEFNLDGAVTANNPTLVAMT 229
QY     217 -----EIHEYNOQLIRKQANKVKLS-----IVVSLGTG 246
Db     230 AVSKQIVKKNPDM-----GKLPGLGDFRFLVISIGTG 261
```

Search completed: May 26, 2005, 14:20:33
Job time : 10.359 secs

A:Cross-references: UNIPROT:Q9YUN7; GB:BA000019; PIDN:BA074001.1; PID:g17131394; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all2302
C:Superfamily: patatin

Query Match 12.9%; Score 198; DB 2; Length 390;
Best Local Similarity 24.3%; Pred. No. 5.1e-10;
Matches 68; Conservative 40; Mismatches 78; Indels 94; Gaps 10;

QY 30 LLCLDGGGVKGLIIQLLIAIEK-----ASGVATKDLFDWVAGTSTGGILALAILHSKSWA 85
Db 5 ILSLDGGGIRGVITARILEVERIOOQQQKSILYEFDLTAGTSTSIITAGIAAKNKS 64
QY 86 YNRGMVFRMKDEVFRGSRP--YESGP-----LEEF-----LKRFGGHTKM 124
Db 65 ELVOLYQEOGKQIFPFRERYKIPSFLOPLIEAFSLPKYSHOGLINVLKVLGD-TR 123
QY 125 TVVRKPKVMLTG-----TLSDRQPAELHLFRNYDAPETVREPRFNQNVN 168
Db 124 KDVESPIMLILAVDTLYRNTFTFNCHPDLDGRWYDDCHL----- 163
QY 169 LRPPAQPSQLVWRAARSSGAPTYFRP-----NGRF--LDGGLLANNPTLDA 214
Db 164 -----WEICTASTAAPTFFPYKLEPVNKEKYNWVFPFHIDGGVAANNPALAA 211
QY 215 MTEIHEYNDLIRKQANKVKLSI-----VVS LGTGRS 248
Db 212 LSLWRLSSVSSAISKQKNLDGINLEDAIILSITGQT 251

RESULT 12
G85437
patatin-like protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: G85437
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: G85437
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-414 <STO>
A:Cross-references: UNIPROT:Q23180; GB:NC_001268; NID:g7270655; PIDN:CAB80372.1; GSPDB:G
A:Gene: AT4g37060
A:Map position: 4
C:Superfamily: patatin

Query Match 11.9%; Score 182; DB 2; Length 414;
Best Local Similarity 27.3%; Pred. No. 1.6e-08;
Matches 73; Conservative 34; Mismatches 84; Indels 76; Gaps 13;

QY 30 LLCLDGGGVKGLIIQLLIAIEK-----ASGVATKDLFDWVAGTSTGGILALAILHSKS 83
Db 21 ILSLDGGGIRGVITARILEVERIOOQQQKSILYEFDLTAGTSTGGILVAMLTPADPE 80
QY 84 MAYMR-----GMVFRMKDEVFRGSRPYESGPLE-----BFLKREFGE 120
Db 81 NGRPRFAAKEIVPFYLEHCKIPF---POPTGVALLPKLXLLSGPKYSGNYLRTLGK 136
QY 121 ----HYKMTDVRKPKVMTLTSLDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSD 177
Db 137 LLGETKLRQLTNVWVTFDIKLTQPT---IFSSYQA---LTPDSLDFKV-----SD 182
QY 178 QLVWRAARSSGAPTYFRP-----NGRFLDGLLANNPTLDAMT-----EIHE 220
Db 183 ICI-----GTSAAPTYPPYFSNEDSQKTRHFNLDVGGVTANNPTLVAMTAVTKQIVN 237
QY 221 YNQDLIRKQANKV-KKLSIVVSLGTG 246

A:Cross-references: UNIPROT:Q23180; GB:NC_001268; NID:g7270655; PIDN:CAB80372.1; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all2302
C:Superfamily: patatin

Db 238 NNPDMD---GTLNPLGYDQFLVISIGTG 261

RESULT 13
F85437
patatin-like protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: F85437
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: F85437
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-428 <STO>
A:Cross-references: UNIPROT:Q23181; GB:NC_001268; NID:g7270654; PIDN:CAB80371.1; GSPDB:G
C:Genetics:
A:Gene: AT4g37050
A:Map position: 4
C:Superfamily: patatin

Query Match 11.7%; Score 179; DB 2; Length 428;
Best Local Similarity 26.5%; Pred. No. 3.1e-08;
Matches 72; Conservative 41; Mismatches 81; Indels 78; Gaps 14;

QY 30 LLCLDGGGVKGLIIQLLIAIEKASGVATK--DLFDWVAGTSTGG-ILALAILHSK 82
Db 37 ILSLDGGGIRGVITARILEVERIOOQQQKSILYEFDLTAGTSTGGILVAMLTAQDQ 96
QY 83 SMAYMRG-----MYFRMKDEVFRGSR-----PYESGPLEEF 113
Db 97 SCGHSNSNRPLFEAKEIVPFYKLSPKLPQPRGIFCGWGTIVLVGGPKFNGKYLHD 156
QY 114 LKREFGEHTMTDVRKPKVMTLTSLDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPA 173
Db 157 LVGEGLDITKLTQSLTNVNVIPCFDIKKLPV---IFSSYQAVN-----NQAMN---A 202
QY 174 QPSDQLVWRAARSSGAPTYFRPNGRF-----LDGGLLANNPTLDAMTEIH 219
Db 203 KLSIDICI-----STSAAPTFF-PAHRFTNEDSEGINHEFNLDGGIAANNPTLCAIAEV- 255
QY 220 EYNQDLIRKQQA-NKVKKLS-----IVVSLGTG 246
Db 256 --TKQIIKKNPVNGDISPLDTRFLVISIGTG 285

RESULT 14
T52294
patatin-like protein [imported] - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C:Accession: T52294
R:Terryn, N.; Heijnen, L.; De Keyser, A.; Van Asseltonck, M.; De Clercq, R.; Verbakel, H.
ueller, C.; Mayer, K.; Dehais, P.; Rombauts, S.; Van Montagu, M.; Rouze, P.; Vos, P.
PEBS Lett. 445, 237-245, 1999
A:Title: Evidence for an ancient chromosomal duplication in Arabidopsis thaliana by seq
A:Reference number: Z26022; MUID:99192287; PMID:10094464
A:Accession: T52294
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-410 <TER>
A:Cross-references: UNIPROT:Q23148; EMBL:AJ002596; PIDN:CAA05628.1
C:Genetics:
A:Map position: 4
C:Superfamily: patatin

Query Match 11.5%; Score 176; DB 2; Length 410;
Best Local Similarity 26.6%; Pred. No. 5.4e-08;
Matches 74; Conservative 36; Mismatches 70; Indels 98; Gaps 15;

QY 30 LLCLDGGGVKGLIIQLLIAIEK-----ASGVATKDLFDWVAGTSTGGILALAILHSKS 83

R.Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Perte, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743; PMID:9804551
A:Accession: G71615
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-679 <GAR>
A:Cross-references: UNIPROT:O96176; GB:AE001393; GB:AE001362; NID:g3845175; PIDN:AAC7187
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0410C

Query Match 13.9%; Score 213.5; DB 2; Length 679;
Best Local Similarity 27.7%; Pred. No. 4.3e-11;
Matches 71; Conservative 37; Mismatches 95; Indels 53; Gaps 8;
QY 30 LILCLDGGGVKGLIIQLLIAIEKASGVATK-----DLFDWVAGTSTGGILALAIL 79
DB 337 ILSLDGGGI---LTISTLLVLRLEAELEKEIGSDDIKLIDCFDMVCGTSGAGLSLALL 393
QY 80 HSKSMAYKGMVFRMKDEVRGSRPVESGPLEE-----ELKREGEHTKMTDVRK 129
DB 394 REIDQVSNMPPSTIKVFEGNRNIISGIFEGVDVNNKDVFLERMGNKF--WSSYKK 451
QY 130 PKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDOLVWRAARSSGA 189
DB 452 FYCFVTATDVHKPKYKFLIRNYTHKYNIAESYDGINKVP-----LWLAAWATAS 503
QY 190 ARTY-----FRNGRFLDGLIANNPTLDAMTEIHEYNQDLIRKQANKV 234
DB 504 APTYLKGPSAEDIKKLGINIKPEIHLVDGALKASNPALTBECARLN---NKNLSTFI 559
QY 235 KK-LSIWSVSLGTGRSP 249
DB 560 KEDLDTLVSIGTGQVP 575

RESULT 9
JC7284
phospholipase A2 (EC 3.1.1.4) 2, calcium-independent - human
N:Alternate names: membrane-associated calcium-independent phospholipase A2
C:Species: Homo sapiens (man)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: JC7284
R:Tanaka, H.; Takeya, R.; Sumimoto, H.
Biochem. Biophys. Res. Commun. 272, 320-326, 2000
A:Title: A novel intracellular membrane-bound calcium-independent phospholipase A2.
A:Reference number: JC7284
A:Accession: JC7284
A:Molecule type: mRNA
A:Residues: 1-782 <TAN>
A:Cross-references: UNIPROT:Q9NP80; DDBJ:AB041261
C:Genetics:
A:Gene: ipla2-2
A:Map position: 7q31
C:Keywords: carboxylic ester hydrolase; membrane-associated protein

Query Match 13.8%; Score 211.5; DB 2; Length 782;
Best Local Similarity 28.5%; Pred. No. 8e-11;
Matches 72; Conservative 33; Mismatches 107; Indels 41; Gaps 8;
QY 16 ILGSRMRDKRTHDLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGIL 75
DB 430 LIGYDVPVKRGIRILSIDGGTGRGVVALQTLKLVLTQKPVHQLFDYICGVSTGAILA 489
QY 76 LAI-LHKSMAVMYRMGMKDEVR-----GSRPYESGPLEEFLKREGEHT 122
DB 490 FMLGLFHMPLDECEELYRKLGSDFVFSQNVIVGVTKMSWSHAFYDSQTWENILKDRMGSA 549
QY 123 KMTDVRK---PKVMLTGTLSDRQ-PAELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQ 178

Db 550 MIETARNPTCPKVAAVSTIVNRGITPKAFVFRNYG-----HPPGINSHY-----LGGCOY 599
QY 179 LVWRAARSSGAAPTYFRP-----NGRFLDGLIANNPTLDAMTEIHEYNQDLIRKQANKV 234
DB 600 KMQAIRASSAAPGYFAEYALGNLDLHQDGLLLNPNPSALAMHECKLWPDV----- 650
QY 235 KKLISIVSLGTGR 247
DB 651 -PLECIVSLGTGR 662

RESULT 10
T48109
hypothetical protein F16M2.50 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T48109
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24459
A:Accession: T48109
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-382 <RIB>
A:Cross-references: UNIPROT:Q9MLW9; EMBL:AL138648
A:Experimental source: cultivar Columbia; BAC clone F16M2
C:Genetics:
A:Map position: 3
A:Introns: 313/3
A:Note: F16M2.50
C:Superfamily: patatin

Query Match 13.1%; Score 201; DB 2; Length 382;
Best Local Similarity 26.7%; Pred. No. 2.7e-10;
Matches 75; Conservative 38; Mismatches 94; Indels 74; Gaps 12;

QY 4 LMHISRAKPAFILGSRMEDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVAT----- 58
DB 19 LSHCDSRK-----TRILSIDGGTGTGIVAAASILHLEHQILQTDGPHA 63
QY 59 --KOLFDMVAGTSTGGILALAILHS-----KSMAYMRGMVFRMK-DEVFRG 101
DB 64 HISDFDIVAGTGTGGILALAILVADGSGRPMFTARDAVKFAEKNSESELFETRYTCVFR 123
QY 102 SRPYESGPLEBFL-----KREFGEHTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPET 157
DB 124 NKRYSGKSMERVLETAFRREDGKVLTKMDTKCPLEVPVPCYDLKTSAP---FVFSRAGASES 180
QY 158 VREPRFNQNVNLRPPAQSDQLVWRAARSSGAAPTYFRP-----NGR-----FLDGLLLA 207
DB 181 ---PSF-----DFELWKVCRATSATPSLFKPFVSVVDGKTSCSAVDGGLVM 224
QY 208 NNPTLDAMTEIHEYNQDLIRKQANKVKKLISIVSLGTGRS 248
DB 225 KNPTAAVTHVLNKRDP---PSVNGVDDL-LVLSLNGGPS 261

RESULT 11
AG2093
patatin-like protein (imported) - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AG2093
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG2093
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-390 <KUR>

A;Reference number: Z14574
A;Accession: T02131
A;Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A;Residues: 1-1265 <YVS>
C;Cross-references: UNIPROT:O80693; EMBL:AC004392; NID:g33282170; PID:g3367519; GSPD:GN00022; CESP:T04B2.5
G;Genetics:
A;Gene: ATSP:F8K4.6
A;Map position: 1
A;Introns: 146/3; 196/1; 229/1; 297/3; 379/3; 434/1; 521/1; 561/3; 615/3; 683/1; 728/3;
C;Superfamily: Arabidopsis thaliana hypothetical protein F8K4.6

Query Match 16.7%; Score 255; DB 2; Length 1265;
Best Local Similarity 28.7%; Pred.No. 1.8e-14;
Matches 81; Conservative 39; Mismatches 90; Indels 72; Gaps 8;

DQ 30 LLCLDGGGVKGILLIIQLLIAIEKASGVATKDLPFWAGTSTGGILALAI-LHKSVMAYR 88
 : : |||::||: |:||||| :||||: |||::||: | :
Db 455 ILTWDDGGMGKLAVQVLKEIKESGPPIHELFDLICGTSTGGMLATAUGVKLTLEQQE 514
 : : |||::||: |:||||| :||||: |||::||: | :

DQ 89 GMFRMKDEVFGRSRP-----YESGP-----LEEFL 113
 : : |||::||: |:||||| :||||: |||::||: | :
Db 515 EIYNKLGKVFAESVPKDNEAAWREXLDQLYKSSQSFRVIHGSKHSANEFERLLKEM 574
 : : |||::||: |:||||| :||||: |||::||: | :

DQ 114 LKRFEGBHTKTMDVRK-PKYMLTGTLSDROPaelHLPRNYDAETVREPFP----NONVN 168
 : : |||::||: |:||||| :||||: |||::||: | :
Db 575 CAEDGDGLLIETAAGNVKPWFVVSTLVSVMPAQPFIFRNYPVGTPEMS YAFSDSHSGS 634
 : : |||::||: |:||||| :||||: |||::||: | :

DQ 169 LRPAQPDSQL-----VRAARSQAAPTYF-----RPNGRFIDGGLLA 207
 : : |||::||: |:||||| :||||: |||::||: | :
Db 635 TLTSSTASDAQGYKOSAFNGCKHQVQMQRASSAAPYYLDDPSFGVTNSYRWODGAIVA 694
 : : |||::||: |:||||| :||||: |||::||: | :

DQ 208 NNPTLDAMTEIHEYNDOLIRKKQANKVKLSIVVSLGTGRSP 249
 : : |||::||: |:||||| :||||: |||::||: | :
Db 695 NNPTIFAIREAQLWPD-----TKIDLVSIGGSVP 726
 : : |||::||: |:||||| :||||: |||::||: | :

RESULT 6
T24442
hypothetical protein T04B2.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24442; T26042
R;Colles, L.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19890
A;Accession: T24442
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A;Residues: 1-456 <WIL>
A;Cross-references: UNIPROT:Q22152; EMBL:Z68299; PIDN:CAA92615.1; GSPDB:GN00022; CESP:T04B2.5
A;Experimental source: clone T04B2
R;Colles, L.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z20141
A;Accession: T26042
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A;Residues: 1-456 <WI2>
A;Cross-references: EMBL:Z68301; PIDN:CAA92628.1; GSPDB:GN00022; CESP:T04B2.5
A;Experimental source: clone W01B6
C;Genetics:
A;Gene: CESP:T04B2.5
A;Map position: 4
A;Introns: 48/3; 104/3; 139/1; 424/3
C;Superfamily: patatin

Query Match 16.6%; Score 253.5; DB 2; Length 456;
Best Local Similarity 32.3%; Pred.No. 5.9e-15;
Matches 86; Conservative 41; Mismatches 76; Indels 63; Gaps 14;

DQ 5 MHISRRARPKAFILGSMERDKTRHDHLLCDLGGGVKGLI-IQLLIAEKASGVAT-KOLF 62
 : : |||::||: |:||||| :||||: |||::||: | :

Db 112 IQINRSKKVDGVMA-----LCLDGGMRGLVSVVCLLYASRRLLDGETLPNLF 159

QY 63 DWAGTSTGGILALAILHKSMAVMRGMVYFMKDEVF-RGSRPYESGPLEEFLKREFGEH 121

Db 160 DWFTGTSTGSMALSMWNKISISECFQYWDKSOIFRGST-----VKRLLDQ 209

QY 122 TKMTDVRKPKVM-----LTGTLSD-----RQPAELHLFRNYDAPETVREPFRN 164

Db 210 VAVQTKNIDKVLGDCFFQTQLQECPTRLTIPALDISTAPARLHVRFNYSFTKPFQCAP-LN 268

QY 165 QVNNLRPPAQSDQVWRAARSSGAAPTYFRP-----NGRFLDGLLANNPTLDAMTEIHE 220

Db 269 ED-----QDVLFRFAARASGAAPTYFBFFIYGNKVLVDGGSFVANYP-LNVL--FK 316

QY 221 YNQDLIRKQANKVKKLSIVVSLGTG 246

Db 317 Y--DSFSKHQ--QPIHLAGVLSIGTG 338

RESULT 7

E82354

patatin-related protein VC0178 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C:Species: Vibrio cholerae

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: E82354

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

harrison, D.; McEwen, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.

l. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: E82354

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-355 <HEI>

A:Cross-references: UNIPROT:Q9KVG8; GB:AE004108; GB:AE003852; NID:g9654578; PIDN:AAF93353

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC0178

A:Map position: 1

C:Superfamily: patatin

Query Match 15.4%; Score 235.5; DB 2; Length 355;

Best Local Similarity 29.2%; Pred. No. 1.8e-13;

Matches 75; Conservative 38; Mismatches 83; Indels 61; Gaps 9;

QY 27 HDHL-----LCLDGGVKGGLIITOLLIAIEK-----ASGVATKDLFDWVAGTSGGI 73

Db 7 YEHLKNQVRILSLNGGARGGLFTISLAEIERIIIEKOGINGFKVGDYFDLITGTSIGGI 66

QY 74 LALAILHKSMAVMRGMV-----FRMKDEVFRGSRPYESGPLEEFL 114

Db 67 LALGLAYCKSARELEDVFRKQAGYIFPEQKYPFRFPFRRYRLARGPL-YDSKPLAKTI 125

QY 115 KRFEGETKMTDVRKPKVMLTGTSLDRQPAELHLFRNYDAPETVREPFRNQVNNLRPPAQ 174

Db 126 ASMVGEESTFNDLRCRVLIPTVNLSTGPK--QQFKTPHNPEFHRDGRK----- 172

QY 175 PSDQLWRAARSSGAAPTYFRP-----NGRFLDGLLANNPTLDAMTEIHEYNQDLIRK 228

Db 173 -----LIDAALATSAAPTYFAPHYCVDLDSYFADGGLVANNP---SFIGLHEVFRDMATD 224

QY 229 QQANKVKKLSIVVSLGT 245

Db 225 FPEAKVSDVKI-LNVGT 240

RESULT 8

G71615

phospholipase A2-like a/b fold hydrolase PFB0410c - malaria parasite (Plasmodium falciparum)

C:Species: Plasmodium falciparum

C>Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004

C:Accession: G71615

A:Accession: T22327
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1071 <W1>
A:Cross-references: UNIPROT:Q20500; EMBL:Z49888; PIDN:CAA90061.1; GSPDB:GN00028; CESP:F47A4
A:Experimental source: Clone F47A4
C:Genetics:
A:Gene: CESP:F47A4.5
A:Map position: X
A:Introns: 27/1; 59/2; 134/1; 199/2; 402/2; 460/3; 591/3; 634/3; 665/2; 1018/3

Query Match 29.8%; Score 456.5; DB 2; Length 1071;
Best Local Similarity 34.5%; Pred. No. 7.4e-33;
Matches 102; Conservative 62; Mismatches 97; Indels 35; Gaps 8;

QY 1 LQDLHISRARKPAFGLSMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
DB 730 IQDTLGGRRGKKAKV-----NLISMDGGGIRGLVITQLLIAIEERLGDIFK 777

QY 61 LFDWAGTSTGGILALAILHSKSMAYMRGMVFRMKDEVPFRG--SRPYESGPLEEFKREGEHTKMTDVRKPKVM 119
DB 778 YFDWSAGTSTGLMAGLATGSLREMQTYLLKDRVFDGIMPYPYDTVQLEKFIQDOFG 837

QY 120 EHTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDOL 179
DB 838 TGT-VWEIPYKIMISAVNSEKLPVRLEWARYKPAKV-----APETPKEMP 884

QY 180 VVRAARSSGAAPTYFRPN--GRFLDGGLLANNPTLDAMTEIHEYNOOLIRKQKVKKLS 238
DB 885 LWMALRRSTAAPVLPKPSREDYIDGGIISNNPALDLMSVHAYNRELQLSGRKSDAVQMN 944

QY 239 IVVSLGTGRSPQVPVTCVDVFR--PSNPWELAKTVFGAKELGKVMVDCCTDPDGRP 292
DB 945 VLVSFQGTG---QTPSTVIETLSIDNSPLQSIKTI----KNLAAMFTDQATASEGAP 994

RESULT 3
T26261
hypothetical protein W07A8.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A:Accession: T26261; T26892
R:Basham, V.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20184
A:Accession: T26261
A:Molecule type: DNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-1023 <W12>
A:Cross-references: UNIPROT:O62398; EMBL:Z82075; PIDN:CAB04932.1; GSPDB:GN00023; CESP:W07A8
A:Experimental source: clone W07A8
R:Ainscough, R.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z20281
A:Accession: T26892
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1023 <W12>
A:Cross-references: EMBL:AL021489; PIDN:CAA16371.1; GSPDB:GN00023; CESP:W07A8.2
A:Experimental source: clone Y44A6C
C:Genetics:
A:Gene: CESP:W07A8.2
A:Map position: 5
A:Introns: 32/1; 83/2; 155/3; 202/2; 240/3; 264/1; 331/2; 411/1; 479/3; 534/3; 571/2; 702/131

Query Match 27.4%; Score 419; DB 2; Length 1023;
Best Local Similarity 33.9%; Pred. No. 1.8e-29;
Matches 95; Conservative 61; Mismatches 110; Indels 14; Gaps 7;

QY 17 LGSMDREKTHD--HLLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWAGTSTGGIL 74
DB 678 LKELVEKKTSNVINVLGDDGGIRGLVTVQMLICLAEFLDRPLIDYFDWIGATSTGCYI 737

QY 75 ALAILHSKSMAYMRGMVFRMKDEVPFRG--SRPYESGPLEEFKREGEHTKMTDVRKPKVM 133
DB 738 MSTMTGSLRKAQRYYLMPFDQDLSDSWTRFYDTKTLETFIQARFAGADRLMGDIKYPRFF 797

QY 134 LTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDOLVVRAARSSGAAPTY 193
DB 798 CTTVRADTFPQLELLRNYRLPISEKE---NNDLGF---TDENELTIWKATERSAAPTY 851

QY 194 FRPN--GRFLDGGLLANNPTLDAMTEIHEYNOOLIRKQKVKKLSIVVSLGTGRSPQVP 252
DB 852 FSASEGKFDIGMISNNPVLDMSDIGFYNTTCQMRIPERKMVDMGCVLSVGTGITPICP 911

QY 253 VTCVDVFRPSNPWELAKTVFGAKELGKVMVDCCTDPDGRP 292
DB 912 VD-PSVFMNDLFGMLR---GMKNLSVLVIDQATATEGAP 947

RESULT 4
T33857
hypothetical protein D1037.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
A:Accession: T33857
R:Ledwith, J.; Biewald, T.
submitted to the EMBL Data Library, November 1998
A:Description: The sequence of C. elegans cosmid D1037.
A:Reference number: Z21424
A:Accession: T33857
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-468 <LED>
A:Cross-references: EMBL:AF106592; PIDN:AAC78490.1; GSPDB:GN00019; CESP:D1037.5
A:Experimental source: strain Bristol N2; clone D1037
C:Genetics:
A:Gene: CESP:D1037.5
A:Map position: 1
A:Introns: 66/3; 89/3; 113/3; 151/2; 247/1; 354/2

Query Match 17.0%; Score 261; DB 2; Length 468;
Best Local Similarity 29.8%; Pred. No. 1.3e-15;
Matches 78; Conservative 54; Mismatches 100; Indels 30; Gaps 10;

QY 16 ILGSMRDEKTHD--LLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWAGTSTGGIL 74
DB 180 VLASEKKQWKPPEERVLALDGGIRAVITIQMLIHIDYLLGGLVEKLLDIAGTSCGGVI 239

QY 75 ALAI--LHSKSMAYMRGMVFRMKDEVP--RGSR---PYESGPLEEFKREF--GEHTKMTDV 127
DB 240 TLLSTNNRNIETKLLIDMRDRVIRGADKAVKYSNGMEYIARHVTWEDSKMSSI 299

QY 128 RPKVYMLTGTLSDRQPAELHLFRNY--DAPETVREP--RFNQNVNLRPPAOPSDQLVWRAA 184
DB 300 KKHRAIVTVADTRMVPPQLLLFRSYRPEMPEACEHYKF-----LDPTKVELWKT 350

QY 185 RSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNOOLIRKQKVKK-----K 236
DB 351 RCTTAAPYFFESFNGSLSDGGLIANNPTLALISDFLTNK--LEKSFASKSSSRERENGNWK 408

QY 237 LSVVSLGTGRSPQVPVTCVDV 258
DB 409 IOCVISLGTGVFPTEKIDGIDL 430

RESULT 5
T02131
hypothetical protein F8K4.6 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
A:Accession: T02131
R:Vystotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Kwan, A.; Yu, G.; Oji, O.; Liu, S.; Li, rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N.
submitted to the EMBL Data Library, August 1998
A:Description: Arabidopsis thaliana chromosome 1 BAC F8K4 sequence.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2005, 14:07:29 ; Search time 8.35905 Seconds
(without alignments)
3361.064 Million cell updates/sec

Title: US-10-612-668-19

Perfect score: 1531

Sequence: 1 LQDLMHISRARKPAFILGSM.....GAKELGKMVVDCTDPDGRP 292

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1524	99.5	851	2 T12503	hypothetical prote
2	456.5	29.8	1071	2 T22327	hypothetical prote
3	419	27.4	1023	2 T26261	hypothetical prote
4	261	17.0	468	2 T33857	hypothetical prote
5	255	16.7	1265	2 T02131	hypothetical prote
6	253.5	16.6	456	2 T24442	hypothetical prote
7	235.5	15.4	355	2 E82354	patatin-related pr
8	213.5	13.9	679	2 G71615	phospholipase A2-1
9	211.5	13.8	782	2 JC7284	phospholipase A2 (
10	201	13.1	382	2 T48109	hypothetical prote
11	198	12.9	390	2 AG2093	patatin-like prote
12	182	11.9	414	2 G85437	patatin-like prote
13	179	11.7	428	2 P85437	patatin-like prote
14	176	11.5	410	2 T52294	patatin-like prote
15	176	11.5	414	2 H85437	patatin-like prote
16	174.5	11.4	390	2 T03841	patatin homolog -
17	164	10.7	499	2 T02580	hypothetical prote
18	163	10.6	405	2 T10260	patatin-like prote
19	161	10.5	407	2 T00989	hypothetical prote
20	158.5	10.4	388	2 T10770	patatin-like latex
21	158.5	10.4	490	2 B97815	patatin bl precurs
22	151.5	9.9	388	2 T10765	patatin-like latex
23	151.5	9.9	388	2 T10765	patatin-like latex
24	150.5	9.8	494	2 D71665	patatin bl precurs
25	147	9.6	526	2 T08541	hypothetical prote
26	146	9.5	386	2 T07592	class I patatin -
27	140	9.1	386	2 A29810	patatin - potato
28	139	9.1	386	2 A26017	patatin T5 precurs
29	138	9.0	377	2 S05593	patatin precursor

30	138	9.0	386	2 S51596	patatin precursor,
31	137	8.9	320	2 F70034	conserved hypothet
32	137	8.9	384	2 A24142	patatin precursor
33	134	8.8	386	2 S05592	patatin precursor
34	134	8.8	386	2 B26017	patatin T58 precur
35	129.5	8.5	488	2 T06725	hypothetical prote
36	124	8.1	318	2 S24923	TEG protein - Bac1
37	116	7.6	324	2 D70943	hypothetical prote
38	112	7.3	473	2 T28118	hypothetical prote
39	108	7.1	329	2 A87087	conserved hypothet
40	103	6.7	610	2 B87518	conserved hypothet
41	96.5	6.3	296	2 E84000	hypothetical prote
42	95	6.2	598	2 E71657	hypothetical prote
43	94	6.1	314	2 AF3365	serine proteinase
44	91	5.9	260	2 H69874	conserved hypothet
45	90.5	5.9	254	2 G72343	conserved hypothet

ALIGNMENTS

RESULT 1

T12503

hypothetical protein DKFp434A102.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999

C;Accession: T12503

R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, June 1999

A;Reference number: Z17527

A;Accession: T12503

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-851 <ANS>

A;Cross-references: EMBL:AL080187

A;Experimental source: adult testis; clone DKFp434A102

C;Genetics:

A;Note: DKFp434A102.1

Query Match 99.5%; Score 1524; DB 2; Length 851;

Best Local Similarity 100.0%; Pred. No. 7.8e-130;

Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	LQDLMHISRARKPAFILGSMRDEKTRHLLCLDGGVKGGLIIQLLIAIEKASGVATKD	60
DB	496	LQDLMHISRARKPAFILGSMRDEKTRHLLCLDGGVKGGLIIQLLIAIEKASGVATKD	555
QY	61	LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGE	120
DB	556	LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGE	615
QY	121	HTKMTDVRPKVMTGTLSDRQPAELHLFRNYDAPETVREPRENQNVNLRPPAQPSDQIV	180
DB	616	HTKMTDVRPKVMTGTLSDRQPAELHLFRNYDAPETVREPRENQNVNLRPPAQPSDQIV	675
QY	181	WRAARSSGAAPTYFRNGRFLDGLIANNPTLDAMTEIHEYNDLIRKQANKVKLSIV	240
DB	676	WRAARSSGAAPTYFRNGRFLDGLIANNPTLDAMTEIHEYNDLIRKQANKVKLSIV	735
QY	241	VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVVDCTDPDGR	291
DB	736	VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVVDCTDPDGR	786

RESULT 2

T22327

hypothetical protein F47A4.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T22327

R;Mortimore, B.

submitted to the EMBL Data Library, June 1995

A;Reference number: Z19549

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-555-568B-2

Query Match      88.1%; Score 1837; DB 2; Length 752;
Best Local Similarity 87.3%; Pred. No. 4.4e-195;
Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTSGVTLNLFSPNPRVKEVAVADYTSSDRVREEGQLILFQNTNRTWDCVLV 60
DB 1 MOFFGRLVNTLSSVTLNLFSPNPRVKEISVADYTSHERVREEGQLILFQNASRTWDCILV 60
QY 61 NPNRSQSGFRLQLELEADALVNFHQYSSQLLPFYESSQVLHTEVLOHLDLIRNHPSW 120
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 120
61 SPRNPHSGFRLQLESEADALVNFQFSSQLPPFYESSQVLHVEVLQHLSDLIRSHPSW 120
QY 121 SVAHLAVELGIRECFPHHSRIISCANCAENEGCTPLHLACRKGDEIILVELVOYCHTQMD 180
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 180
121 TVTHLAVELGIRECFPHHSRIISCANSTENEGCTPLHLACRKGDEIILVELVOYCHTQMD 180
QY 181 VTDYKGTVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGQKQEMVRVLL 240
DB 181 VTDNKGETAHYAVQGDNSQVLQLGKNASAGLNQVNNQGLTPLHLACQMGQKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAKFQSGKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 300
241 LCNARCNVMGSPGPIHTAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLXRGCVNVTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRGCDVDS TSAAGNTALHVAVMNRFDCAIVLLTHGANADARGEHNTPLHLAISK 360
QY 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKI 393
DB 361 DNMEMIKALIVFGAEVDTNDFGETPAFWASKI 393

RESULT 15
US-09-519-223-2
; Sequence 2, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
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;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-519-223-2

Query Match      88.1%; Score 1837; DB 3; Length 752;
Best Local Similarity 87.3%; Pred. No. 4.4e-195;
Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTSGVTLNLFSPNPRVKEVAVADYTSSDRVREEGQLILFQNTNRTWDCVLV 60
DB 1 MOFFGRLVNTLSSVTLNLFSPNPRVKEISVADYTSHERVREEGQLILFQNASRTWDCILV 60
QY 61 NPNRSQSGFRLQLELEADALVNFHQYSSQLLPFYESSQVLHTEVLOHLDLIRNHPSW 120
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 120
61 SPRNPHSGFRLQLESEADALVNFQFSSQLPPFYESSQVLHVEVLQHLSDLIRSHPSW 120
QY 121 SVAHLAVELGIRECFPHHSRIISCANCAENEGCTPLHLACRKGDEIILVELVOYCHTQMD 180
DB 121 TVTHLAVELGIRECFPHHSRIISCANSTENEGCTPLHLACRKGDEIILVELVOYCHTQMD 180
QY 181 VTDYKGTVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGQKQEMVRVLL 240
DB 181 VTDNKGETAHYAVQGDNSQVLQLGKNASAGLNQVNNQGLTPLHLACQMGQKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAKFQSGKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 300
241 LCNARCNVMGSPGPIHTAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLXRGCVNVTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRGCDVDS TSAAGNTALHVAVMNRFDCAIVLLTHGANADARGEHNTPLHLAISK 360
QY 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKI 393
DB 361 DNMEMIKALIVFGAEVDTNDFGETPAFWASKI 393

Search completed: May 26, 2005, 14:21:56
Job time : 20.5289 secs
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QY 361 DNMEMIKALIVFGAEVDTNDGFTPTFLASKI 393
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Db 361 DNMEMIKALIVFGAEVDTNDGFTPTAFWASKI 393
||:|||||

RESULT 12

US-08-422-106-2

; Sequence 2, Application US/08422106

; Patent No. 5589170

; GENERAL INFORMATION:

; APPLICANT: Jones, Simon

; APPLICANT: Tang, Jim

; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

; NUMBER OF SEQUENCES: 15

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/422,106

; FILING DATE: 14-APR-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/281,193

; FILING DATE: 27-JUL-1994

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 752 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-422-106-2

Query Match

Best Local Similarity 88.1%; Score 1837; DB 1; Length 752;

; Sequence 2, Application US/08735716

; Patent No. 5840511

; GENERAL INFORMATION:

; APPLICANT: Jones, Simon

; APPLICANT: Tang, Jim

; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

; NUMBER OF SEQUENCES: 15

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/422,106

; FILING DATE: 14-APR-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/281,193

; FILING DATE: 27-JUL-1994

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 752 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-422-106-2

Query Match

Best Local Similarity 88.1%; Score 1837; DB 1; Length 752;

; Sequence 2, Application US/08735716

; Patent No. 5840511

; GENERAL INFORMATION:

; APPLICANT: Jones, Simon

; APPLICANT: Tang, Jim

; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

; NUMBER OF SEQUENCES: 15

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/422,106

; FILING DATE: 14-APR-1995

; CLASSIFICATION: 435

QY

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US-09-927-180-23

Query Match 100.0%; Score 2084; DB 4; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTLNFSNPRVKEVAVADYSSDRVREEGQLILFQNTNRTWDCVLV 60
DB 1 MOFFGRLVNTFSGVTLNFSNPRVKEVAVADYSSDRVREEGQLILFQNTNRTWDCVLV 60
QY 61 NPNRSQSGFRLQLELEADALVNFHQSOLLPPFYESSQVLHTEVQLHLDLIRNHPSW 120
DB 61 NPNRSQSGFRLQLELEADALVNFHQSOLLPPFYESSQVLHTEVQLHLDLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVOGDINSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVOGDINSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNTMGPNYPIHSAKFESQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEWA 300
DB 241 LCNARCNTMGPNYPIHSAKFESQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEWA 300
QY 301 RMLLRKGCNVNSTSAGNTALHVGVMRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRKGCNVNSTSAGNTALHVGVMRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIG 394

RESULT 10

US-09-949-016-10948
; Sequence 10948, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10948
; LENGTH: 819
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10948

Query Match 99.7%; Score 2078; DB 4; Length 819;
Best Local Similarity 99.7%; Pred. No. 7.5e-222;
Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTLNFSNPRVKEVAVADYSSDRVREEGQLILFQNTNRTWDCVLV 60
DB 14 MOFFGRLVNTFSGVTLNFSNPRVKEVAVADYSSDRVREEGQLILFQNTNRTWDCVLV 73
QY 61 NPNRSQSGFRLQLELEADALVNFHQSOLLPPFYESSQVLHTEVQLHLDLIRNHPSW 120
DB 74 NPNRSQSGFRLQLELEADALVNFHQSOLLPPFYESSQVLHTEVQLHLDLIRNHPSW 133
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 180

DB 134 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 193
QY 181 VTDYKGETVFHYAVOGDINSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 194 VTDYKGETVFHYAVOGDINSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 253
QY 241 LCNARCNTMGPNYPIHSAKFESQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEWA 300
DB 254 LCNARCNTMGPNYPIHSAKFESQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEWA 313
QY 301 RMLLRKGCNVNSTSAGNTALHVGVMRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 314 RMLLRKGCNVNSTSAGNTALHVGVMRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 373
QY 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIG 394
DB 374 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIG 407

RESULT 11

US-08-281-193-2
; Sequence 2, Application US/08281193
; Patent No. 5466595
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-281-193-2

Query Match 88.1%; Score 1837; DB 1; Length 752;
Best Local Similarity 87.3%; Pred. No. 4.4e-195;
Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTLNFSNPRVKEVAVADYSSDRVREEGQLILFQNTNRTWDCVLV 60
DB 1 MOFFGRLVNTLSSVTNLFNFSNPRVKEISVADYTSHERVREEGQLILFQNASNRTWDCILV 60
QY 61 NPNRSQSGFRLQLELEADALVNFHQSOLLPPFYESSQVLHTEVQLHLDLIRNHPSW 120
DB 61 SPRNPHSGFRLQLESEADALVNFQFSQPPFYESSQVLHVEVQLHSLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 180
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRKGDSLEILVELVQYCHQMD 180
QY 181 VTDYKGETVFHYAVOGDINSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDNKGETAFAHYAVOGDINSQVLQLGKNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
QY 241 LCNARCNTMGPNYPIHSAKFESQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEWA 300
DB 241 LCNARCNTMGSPGPIHTAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEWA 300
QY 301 RMLLRKGCNVNSTSAGNTALHVGVMRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRKGCVDVSTSAAGNTALHVAVMRNFDCVWLLTYGANAGTGEHNTPLHLAISK 360

Qy	1	MOFFGRLVNTFGSVTNLFSNPRVKVAVADYTSSDRVREGQLILFQNTPNRTWDCVLV	60
Db	1	MQFFGRLVNTFGSVTNLFSNPRVKVAVADYTSSDRVREGQLILFQNTPNRTWDCVLV	60
Qy	61	NPNRSQSGRLFQLEADALVNFHQYSSQLLPYESSQVLVHTEVLQHLTDLIRNHPSW	120
Db	61	NPNRSQSGRLFQLEADALVNFHQYSSQLLPYESSQVLVHTEVLQHLTDLIRNHPSW	120
Qy	121	SVAHLAVELIGIRECFHHSRIISCANCAENEGCTPLHLACRKGDETLVELVOYCHTQMD	180
Db	121	SVAHLAVELIGIRECFHHSRIISCANCAENEGCTPLHLACRKGDETLVELVOYCHTQMD	180
Qy	181	VTDYKGETVFHYAVQDINSQVLLQLGRAVAGLVQVNNQGLTPHLACQLGKGEMVRVLL	240
Db	181	VTDYKGETVFHYAVQDINSQVLLQLGRAVAGLVQVNNQGLTPHLACQLGKGEMVRVLL	240
Qy	241	LCNARCINMGPGYPIHSAKFSQKGCACMIISMDSSQIHSKDPRYGASPLHWAKNAEMA	300
Db	241	LCNARCINMGPGYPIHSAKFSQKGCACMIISMDSSQIHSKDPRYGASPLHWAKNAEMA	300
Qy	301	RMLLRKGCNVNSTSSAGNTALHVGVMNRPFCAIVLLTHGANADARGEHNTPLHLAMSK	360
Db	301	RMLLRKGCNVNSTSSAGNTALHVGVMNRPFCAIVLLTHGANADARGEHNTPLHLAMSK	360
Qy	361	DNVEMIKALIVFGAEVDTNDPGETPTPLASKIG	394
Db	361	DNVEMIKALIVFGAEVDTNDPGETPTPLASKIG	394

RESULT 8

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US-09-519-223-23
; Sequence 23, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-519-223-23

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Query Match

100.0%; Score 2084; DB 3; Length 688;

Best Local Similarity 100.0%; Pred. No. 1.2e-222;		
Matches 394;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MQPFGRLVNTFSQVTLFNSNPRVKAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
Db	1	MQPFGRLVNTFSQVTLFNSNPRVKAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
Qy	61	NPNNSQSGFRLFOLELEADALVNFHQYSSQLLPFYESSQVHLTEVLOHLTLDIRNHPSW 120
Db	61	NPNNSQSGFRLFOLELEADALVNFHQYSSQLLPFYESSQVHLTEVLOHLTLDIRNHPSW 120
Qy	121	SVAHLAVELGIRECFPHHSRIISCANCAENEEGCTPLHLACRKGDGEILVELVOYCHTQMD 180
Db	121	SVAHLAVELGIRECFPHHSRIISCANCAENEEGCTPLHLACRKGDGEILVELVOYCHTQMD 180
Qy	181	VTDTKGETVPHYAVQCDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
Db	181	VTDTKGETVPHYAVQCDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
Qy	241	LCNARCNIIMGPGYPIHSAWKSQKCAEMIISMDSQIHSKDPRYGASPLHWAKNAEMA 300
Db	241	LCNARCNIIMGPGYPIHSAWKSQKCAEMIISMDSQIHSKDPRYGASPLHWAKNAEMA 300
Qy	301	RMLLKEGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHGNTPHLAMSK 360
Db	301	RMLLKEGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHGNTPHLAMSK 360
Qy	361	DNVEMIKALIVFGAEVDTNDFGETPTFLASKIG 394
Db	361	DNVEMIKALIVFGAEVDTNDFGETPTFLASKIG 394

RESULT 9

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US-09-927-180-23
; Sequence 23, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
;
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:

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Db 1 MQFFGRLVNTFSVNTLFSNPNFRVKEVAVADYTSDDRVREBQQLILFQNTPNRTWDCVILV 60
QY 61 NPRNSQSGFRLFOLEADALVNFHQSOLLPPFYESSQVILHTEVLOHLTDLIRNHPWS 120
Db 61 NPRNSQSGFRLFOLEADALVNFHQSOLLPPFYESSQVILHTEVLOHLTDLIRNHPWS 120
QY 121 SVLAHVELGIRECFPHHSRIISCANCAENEGECTPLHLACRKGDEIILVELVOYCHTQMD 180
Db 121 SVLAHVELGIRECFPHHSRIISCANCAENEGECTPLHLACRKGDEIILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNIIMPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPRYGASPLHWAKNAEMA 300
Db 241 LCNARCNIIMPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPRYGASPLHWAKNAEMA 300
QY 301 RMLLRKGCNVNSTSSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHGNTPHLAMSK 360
Db 301 RMLLRKGCNVNSTSSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHGNTPHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDFGPTFLASKIG 394
Db 361 DNVEMIKALIVFGAEVDTNDFGPTFLASKIG 394

RESULT 6
US-09-927-180-21
; Sequence 21, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match 100.0%; Score 2084; DB 4; Length 687;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQFFGRLVNTFSVNTLFSNPNFRVKEVAVADYTSDDRVREBQQLILFQNTPNRTWDCVILV 60
Db 1 MQFFGRLVNTFSVNTLFSNPNFRVKEVAVADYTSDDRVREBQQLILFQNTPNRTWDCVILV 60
QY 61 NPRNSQSGFRLFOLEADALVNFHQSOLLPPFYESSQVILHTEVLOHLTDLIRNHPWS 120
Db 61 NPRNSQSGFRLFOLEADALVNFHQSOLLPPFYESSQVILHTEVLOHLTDLIRNHPWS 120
QY 121 SVLAHVELGIRECFPHHSRIISCANCAENEGECTPLHLACRKGDEIILVELVOYCHTQMD 180
Db 121 SVLAHVELGIRECFPHHSRIISCANCAENEGECTPLHLACRKGDEIILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNIIMPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPRYGASPLHWAKNAEMA 300
Db 241 LCNARCNIIMPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPRYGASPLHWAKNAEMA 300
QY 301 RMLLRKGCNVNSTSSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHGNTPHLAMSK 360
Db 301 RMLLRKGCNVNSTSSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHGNTPHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDFGPTFLASKIG 394
Db 361 DNVEMIKALIVFGAEVDTNDFGPTFLASKIG 394

RESULT 7
US-08-555-568B-23
; Sequence 23, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-555-568B-23

Query Match 100.0%; Score 2084; DB 2; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MOFFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60

QY 61 NPNRSQSGRLFOLELEADALVNFHOYSSQLLPFYESSPOVLHTEVLQHLTDLIRNHPSW 120

Db 61 NPNRSQSGRLFOLELEADALVNFHOYSSQLLPFYESSPOVLHTEVLQHLTDLIRNHPSW 120

QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDGGEILVELVQYCHTQMD 180

Db 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDGGEILVELVQYCHTQMD 180

QY 181 VTDYKGETVFHYAVQDGNQSVQLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

Db 181 VTDYKGETVFHYAVQDGNQSVQLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

QY 241 LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSSQIHSKDPRYGASPLHWAKNAEMA 300

Db 241 LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSSQIHSKDPRYGASPLHWAKNAEMA 300

QY 301 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHGNTPLHLAMSK 360

Db 301 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHGNTPLHLAMSK 360

QY 361 DNVEMIKALIVFGAEVDTNDFGCTPTFLASKIG 394

Db 361 DNVEMIKALIVFGAEVDTNDFGCTPTFLASKIG 394

RESULT 4

US-08-555-568B-21

Sequence 21, Application US/08555568B

Patent No. 5976854

GENERAL INFORMATION:

APPLICANT: Jones, Simon

APPLICANT: Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/555,568B

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 687 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-555-568B-21

Query Match 100.0%; Score 2084; DB 2; Length 687;

Best Local Similarity 100.0%; Pred. No. 1.2e-222;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60

Db 1 MOFFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60

QY 61 NPNRSQSGRLFOLELEADALVNFHOYSSQLLPFYESSPOVLHTEVLQHLTDLIRNHPSW 120

Db 61 NPNRSQSGRLFOLELEADALVNFHOYSSQLLPFYESSPOVLHTEVLQHLTDLIRNHPSW 120

QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDGGEILVELVQYCHTQMD 180

Db 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDGGEILVELVQYCHTQMD 180

QY 181 VTDYKGETVFHYAVQDGNQSVQLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

Db 181 VTDYKGETVFHYAVQDGNQSVQLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

QY 241 LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSSQIHSKDPRYGASPLHWAKNAEMA 300

Db 241 LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSSQIHSKDPRYGASPLHWAKNAEMA 300

QY 301 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHGNTPLHLAMSK 360

Db 301 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHGNTPLHLAMSK 360

QY 361 DNVEMIKALIVFGAEVDTNDFGCTPTFLASKIG 394

Db 361 DNVEMIKALIVFGAEVDTNDFGCTPTFLASKIG 394

RESULT 5

US-09-519-223-21

Sequence 21, Application US/09519223

Patent No. 6274140

GENERAL INFORMATION:

APPLICANT: Jones, Simon

APPLICANT: Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/519,223

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/555,568

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 687 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-519-223-21

Query Match 100.0%; Score 2084; DB 3; Length 687;

Best Local Similarity 100.0%; Pred. No. 1.2e-222;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60

QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVOGDNSQVLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVOGDNSQVLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPHYGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPHYGASPLHWAKNAEMA 300
QY 301 RMLLRKGCNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRKGCNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394

RESULT 2

US-09-519-223-17
; Sequence 17, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-519-223-17

Query Match 100.0%; Score 2084; DB 3; Length 394;
Best Local Similarity 100.0%; Pred. No. 5e-223;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTNLFNPNFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVILV 60
DB 1 MOFFGRLVNTFSGVTNLFNPNFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVILV 60
QY 61 NPNRSQSGRLFQLEADALVNFHOYSSQLLPFYESSQVLHTEVLOHLDLIRNHPSW 120

DB 61 NPNRSQSGRLFQLEADALVNFHOYSSQLLPFYESSQVLHTEVLOHLDLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVOGDNSQVLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVOGDNSQVLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPHYGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPHYGASPLHWAKNAEMA 300
QY 301 RMLLRKGCNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRKGCNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394

RESULT 3

US-09-927-180-17
; Sequence 17, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-927-180-17

Query Match 100.0%; Score 2084; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 5e-223;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTNLFNPNFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVILV 60

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:08:24 ; Search time 14.5289 Seconds
(without alignments)
2024.365 Million cell updates/sec

Title: US-10-612-668-17
Perfect score: 2084
Sequence: 1 MOFFGRLVNTFGVNTLFSN.....EVDTPNDFGTPTFLASKIG 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2084	100.0	394	2	US-08-555-568B-17
2	2084	100.0	394	3	US-09-519-223-17
3	2084	100.0	394	4	US-09-927-180-17
4	2084	100.0	687	2	US-08-555-568B-21
5	2084	100.0	687	3	US-09-519-223-21
6	2084	100.0	687	4	US-09-927-180-21
7	2084	100.0	688	2	US-08-555-568B-23
8	2084	100.0	688	3	US-09-519-223-23
9	2084	100.0	688	4	US-09-927-180-23
10	2078	99.7	819	4	US-09-949-016-10948
11	1837	88.1	752	1	US-08-281-193-2
12	1837	88.1	752	2	US-08-422-106-2
13	1837	88.1	752	2	US-08-735-716-2
14	1837	88.1	752	2	US-08-555-568B-2
15	1837	88.1	752	3	US-09-519-223-2
16	1837	88.1	752	4	US-09-927-180-2
17	1837	88.1	752	5	PCT-US95-08069-2
18	494.5	23.7	896	4	US-09-270-767-46130
19	359.5	17.3	545	4	US-09-270-767-61684
20	338	16.2	843	2	US-09-172-977-3
21	338	16.2	843	3	US-09-404-108-3
22	332	15.9	1839	2	US-09-172-977-4
23	332	15.9	1839	4	US-09-404-108-4
24	332	15.9	2753	4	US-09-949-016-7659
25	332	15.9	2753	4	US-09-949-016-7660
26	332	15.9	3924	4	US-09-538-092-1246
27	305.5	14.7	1745	2	US-09-031-485-33

28	305.5	14.7	1745	2	US-08-847-429A-33	Sequence 33, Appl
29	305.5	14.7	1745	3	US-09-065-474-33	Sequence 33, Appl
30	305.5	14.7	1745	3	US-09-557-034-33	Sequence 33, Appl
31	301	14.4	786	4	US-09-509-802-2	Sequence 2, Appl
32	301	14.4	787	3	US-09-188-930-334	Sequence 334, App
33	301	14.4	787	4	US-09-312-283C-334	Sequence 334, App
34	296	14.2	1088	3	US-09-082-059-2	Sequence 2, Appl
35	296	14.2	3913	4	US-09-949-016-10933	Sequence 10933, A
36	296	14.2	4377	4	US-09-949-016-6978	Sequence 6978, Ap
37	294	14.1	1719	4	US-09-949-016-6966	Sequence 6966, Ap
38	294	14.1	1856	4	US-09-949-016-6964	Sequence 6964, Ap
39	294	14.1	1880	4	US-09-949-016-5876	Sequence 5876, Ap
40	294	14.1	1881	4	US-09-949-016-6965	Sequence 6965, Ap
41	294	14.1	1883	4	US-09-949-016-9010	Sequence 9010, Ap
42	294	14.1	1883	4	US-09-949-016-9011	Sequence 9011, Ap
43	294	14.1	1883	4	US-09-949-016-9012	Sequence 9012, Ap
44	294	14.1	1883	4	US-09-949-016-9013	Sequence 9013, Ap
45	294	14.1	1883	4	US-09-949-016-9014	Sequence 9014, Ap

ALIGNMENTS

RESULT 1
US-08-555-568B-17
; Sequence 17, Application US/085555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-17

Query Match	100.0%;	Score 2084;	DB 2;	Length 394;
Best Local Similarity	100.0%;	Pred. No. 5e-223;		
Matches 394;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MOFFGRLVNTFGVNTLFSNPRVKEVAVADYTSDDRVREEGOLILFQNTPNRTWDCVLV	60	
Db	1	MOFFGRLVNTFGVNTLFSNPRVKEVAVADYTSDDRVREEGOLILFQNTPNRTWDCVLV	60	
QY	61	NPRNSQSGFRLFQLEADALVNFHQYSSQLLPFYESSPOVLHTEVLOHLTDLIRNHPWS	120	
Db	61	NPRNSQSGFRLFQLEADALVNFHQYSSQLLPFYESSPOVLHTEVLOHLTDLIRNHPWS	120	

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Db 176 QRGHYRVARILIDLCSDWICSLQAQTPLHVAETGHTSTARLLHRGAKZALTSEGYT 235
QY 353 PLHLAMSKDNVEMIKALIVFGAEVDTPDNDFGETPTFLASKIG 394
Db 236 ALHLAAQNGHLATVKKLIEEKADVMARGPLNQJLHLLAAARG 277

RESULT 15

US-09-964-899-43
; Sequence 43, Application US/09964899
; Patent No. US20020174446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; FILE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 1724
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-964-899-43

Query Match 14.4%; Score 300.5; DB 9; Length 1724;
Best Local Similarity 28.4%; Pred. No. 4.8e-19;
Matches 85; Conservative 71; Mismatches 120; Indels 23; Gaps 10;
QY 106 VLOH---LTDLRNHPWSVAHLAVELGIRECPH--SRIISCANCAENEE---GCTPLH 157
Db 315 LLQHNVPDVTNDY--LTALHVA-----HCGHYKVKVLLDKANPNKALNGFTPLH 367
QY 158 LACRKGDELVELVOYCHTQMDVTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNQVN 217
Db 368 IACKNRKIKWELLKHGASIQAVTE-RGETALHMAARSGQAEVVRVLYODG-AQVEAKA 425
QY 218 NOGLTPLHLACQLGKQEMVRVLLLCNARCNIMGPNGY-PIHSAMKFSQKCAEMIISMS 276
Db 426 KODQTEPLHISARLGKADIQQLLQOGASPNAAATSGYTPHLRSAREGHEDVAFLDHGA 485
QY 277 SQIHSKDPRYGASPLHWA---KVAENARMLLKRGCVNNSTSSAGNTALHVGWNRNRPDCA 333
Db 486 SL--SITTKSGLTPLHVAHYDNQKVALLLDQGASPHAAAKNGYTPHLIAAKNQMDIA 543
QY 334 IVLLTHGANADARGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTPDNDFGETPTFLASK 392
Db 544 TTLLEYGADANAVTROGIASVHLAAQEGHVDWVLSLLGRNANVNLNSKSGLTPLHLAAQ 602

Search completed: May 26, 2005, 14:51:02
Job time : 61.7186 secs


```
; SEQ ID NO 2
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-299-327-2

Query Match      14.4%; Score 301; DB 14; Length 786;
Best Local Similarity 31.8%; Pred. No. 1.4e-19;
Matches 92; Conservative 48; Mismatches 137; Indels 12; Gaps 8;

QY 112 DLIRNHPMSVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLAC-RKGDGEILVE 170
Db 434 DLVLD-SSASLLHLAVEAGQEECVKWLNNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
QY 171 LVQYCHTQMDVTDYKGETVFHYAVQ-GDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQ 229
Db 491 LLLARKTSVNAKDEQWTALHFAAQNGDEASTRLLEKN--ASVNEVDPEGRTPMHVACQ 548
QY 230 LKQEMVRVLLLCNARCNIIMGPNY-PIHSAMKFSQKGAEMIISMDSQIHSKDPRYGA 288
Db 549 HQENIVRTLRRGVGVGQGDWALPLHYAAWQGHLPVIVKLLAKQPGVSVNAQ-TLDGR 607
QY 289 SPLHWAK---NAEMARMILKRCNVNSTSSAGNTALHVGVMNRFPDCAIVLLTHGANADA 345
Db 608 TPLHLAAQGRHYRVARILDLCSQVNICSLQACTPLHVAETGHTSTARLLHHRGAGKEA 667
QY 346 RGEHGNTPHLAMSKDNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394
Db 668 LTSEGYTALHAAQNGHLATVLLIEEKADVMARGPLNQTLHLAAARG 716

RESULT 9
US-10-128-174-13
; Sequence 13, Application US/10128174
; Publication No. US20030199462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-128-174-13

Query Match      14.4%; Score 301; DB 14; Length 786;
Best Local Similarity 31.8%; Pred. No. 1.4e-19;
Matches 92; Conservative 48; Mismatches 137; Indels 12; Gaps 8;

QY 112 DLIRNHPMSVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLAC-RKGDGEILVE 170
Db 434 DLVLD-SSASLLHLAVEAGQEECVKWLNNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
QY 171 LVQYCHTQMDVTDYKGETVFHYAVQ-GDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQ 229
Db 491 LLLARKTSVNAKDEQWTALHFAAQNGDEASTRLLEKN--ASVNEVDPEGRTPMHVACQ 548
QY 230 LKQEMVRVLLLCNARCNIIMGPNY-PIHSAMKFSQKGAEMIISMDSQIHSKDPRYGA 288
Db 549 HQENIVRTLRRGVGVGQGDWALPLHYAAWQGHLPVIVKLLAKQPGVSVNAQ-TLDGR 607
QY 289 SPLHWAK---NAEMARMILKRCNVNSTSSAGNTALHVGVMNRFPDCAIVLLTHGANADA 345
Db 608 TPLHLAAQGRHYRVARILDLCSQVNICSLQACTPLHVAETGHTSTARLLHHRGAGKEA 667
QY 346 RGEHGNTPHLAMSKDNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394
Db 668 LTSEGYTALHAAQNGHLATVLLIEEKADVMARGPLNQTLHLAAARG 716

RESULT 10
US-10-128-174-31
; Sequence 31, Application US/10128174
; Publication No. US20030199462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 31
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-128-174-31

Query Match      14.4%; Score 301; DB 14; Length 786;
Best Local Similarity 31.8%; Pred. No. 1.4e-19;
Matches 92; Conservative 48; Mismatches 137; Indels 12; Gaps 8;

QY 112 DLIRNHPMSVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLAC-RKGDGEILVE 170
Db 434 DLVLD-SSASLLHLAVEAGQEECVKWLNNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
QY 171 LVQYCHTQMDVTDYKGETVFHYAVQ-GDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQ 229
Db 491 LLLARKTSVNAKDEQWTALHFAAQNGDEASTRLLEKN--ASVNEVDPEGRTPMHVACQ 548
QY 230 LKQEMVRVLLLCNARCNIIMGPNY-PIHSAMKFSQKGAEMIISMDSQIHSKDPRYGA 288
Db 549 HQENIVRTLRRGVGVGQGDWALPLHYAAWQGHLPVIVKLLAKQPGVSVNAQ-TLDGR 607
QY 289 SPLHWAK---NAEMARMILKRCNVNSTSSAGNTALHVGVMNRFPDCAIVLLTHGANADA 345
Db 608 TPLHLAAQGRHYRVARILDLCSQVNICSLQACTPLHVAETGHTSTARLLHHRGAGKEA 667
QY 346 RGEHGNTPHLAMSKDNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394
Db 668 LTSEGYTALHAAQNGHLATVLLIEEKADVMARGPLNQTLHLAAARG 716

RESULT 11
US-10-128-174-32
; Sequence 32, Application US/10128174
; Publication No. US20030199462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 32
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-128-174-32

Query Match      14.4%; Score 301; DB 14; Length 786;
Best Local Similarity 31.8%; Pred. No. 1.4e-19;
Matches 92; Conservative 48; Mismatches 137; Indels 12; Gaps 8;

QY 112 DLIRNHPMSVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLAC-RKGDGEILVE 170
Db 434 DLVLD-SSASLLHLAVEAGQEECVKWLNNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
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Db	1	MQPFGELVNTFSGVNTLFSNPRVKEVAVADYTSDDRVRREGQILIFQNTPNRTWDCVLV	60
Qy	61	NPRNSQSGFRLFQLEADALVNFHQYSSQLLPFYESSQVLVTEVLQHLTDIRNHPSW	120
Db	61	YPRNSQSGFRLFQLEADALVNFHQYSS-----	89
Qy	121	SVANHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACKRGDGEILVELVOYCHTQMD	180
Db	90	-----	89
Qy	181	VTDYKGETVFHYAVOGDINSQVLLQLGRNAVAGLNOVNNQGLTPLHLACOLGKQEMVRVLL	240
Db	90	-----QLGKQEMVRVLL	101
Qy	241	LCNARCNIMGPNGYPIHSAMKFSQKGCACMIISMDSSQIHSKDPRYGASPLHWAKVAEMA	300
Db	102	LCNARCNIMGPNGYPIYSAMKFSQKGCACMIISMDSSQIHSKDPRYGASPLHWAKVAEMA	161
Qy	301	RMLLKRGCVNSTSSAGNTALHVGVMNRNRFDCAIVLLTHGANADARGEHGNTPLHLSMSK	360
Db	162	RMLLKRGCVNSTSSAGNTALHVAVMNRNRFDCAIVLLTHGANADARGEHGNTPLHLSMSK	221
Qy	361	DNVEMIKALIVFGAEVDTNPDFGPTPTFLASKIG	394
Db	222	DNVEMIKALIVFGAEVDTNPDFGPTPTFLASKIG	255

RESULT 6

US-10-108-260A-3237
; Sequence 3237, Application US/10108260A
; Publication No. US20040005560A1

```

; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patent Ver. 2.1

```

Query Match	15.5%	Score 324;	DB 15;
Best Local Similarity	27.0%	Pred. No. 1.8e-21;	Length 1330;
Matches 99;	Conservative 62;	Mismatches 128;	Indels 77;
			Gaps 9;

Qy 175 ----CH-----TQMDVTDYKGETVFHYAVQGDNSQVLQLLGRNAVAG 212
|
|||:|||||:|:|:|
Db 410 GLTPIHVAAPMGHUNIVLLLLQNGASPDVTNIRGETALHVAARAGQEVVRCLLRG-AL 468

Qy 272 ISMDSSQIHSKDPYGPASPLHWAK---NAEWARMLLKRGCVNVNSTSSAGNTALHVGVMRN 328
::: || : ||| : : : ||| : : : ||| : : : ||| :
Db 529 --LEAGAHSLSATKSGFTPLHVAAKYGSIDVAKLLPDRRAADSAGNIGLTPHVAAYD 586

Qy	389	LASKIG	394
		:	
Db	647	LASQEG	652

RESULT 7

US-10-164-080-2
; Sequence 2, Application US/10164080
; Publication No. US20030087411A1

```

: GENERAL INFORMATION:
: APPLICANT: BIRD, Timothy, A. M.
: APPLICANT: HOLLAND, Pamela, J.
: APPLICANT: PESCHON, Jacques, J.
: APPLICANT: VIRCA, George, D.
: TITLE OF INVENTION: DEATH ASSOCI
: TITLE OF INVENTION: USE

```

Query Match	14.4%;	Score 301;	DB 14;	Length 786;
Best Local Similarity	31.8%;	Pred. No. 1.4e-19;		
Matches 92;	Conservative 48;	Mismatches 137;	Indels 12;	Gaps 8;

y
b

171 LVQYCHTQMVDVTDYKGETVFHYAVQ-GDNSQVLQLGRNAVAGLNQNQGILTPHLACQ 229
| : | : | : | : | : | : | : | : | : | : | : | : | : |
491 LLLARKTSVNAKDEOWTALHFAAQNGDEASTRILLEKN--ASVNEVDFEGRTPMHVACQ 548

289 SPLHWAK--NAEMARMILLKRGCCNVNSTSSAGNTALHVGVNRNRPDCAIVLLTHGANADA 345
:||| : :||| : ||| : ||| : ||| :
608 TPLHLAORGHYRVARILIDLCSDVNICSLAOOTPLHVAETGHTSTARLLHRGAGKEA 667

RESULT 8

US-10-299-327-2
; Sequence 2, Application US/10299327
; Publication No. US20030104482A1

GENERAL INFORMATION:
APPLICANT: Immunex Corp.
APPLICANT: Bird, Timothy
APPLICANT: Virca, G.D.
TITLE OF INVENTION: DEATH-
TITLE OF INVENTION: (DAK)
FILE REFERENCE: 2889-IJS

```

; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
;   NAME: Brown, Scott A.
;   TELEPHONE: (617) 498-8224
;   TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 688 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-927-180-23

Query Match      100.0%; Score 2084; DB 9; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.1e-130;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY    1 MQFFGLVNTFSGVNLFNSNPFRVKEAVADYTSSDRVRREGQLILFQNTPNRTWDCVLV 60
DB    1 MQFFGRLVNTLSSVTNLFSNPFRVKEISVDYTSHERVREBQQLILFQNASRNTWDCLV 60
QY    61 NPNRSOSGRFLFOLEADALVNPHOYSSQLLPFYESSPQVLHTEVLOHLTDLIRNHPWS 120
DB    61 NPNRSOSGRFLFOLEADALVNPHOYSSQLLPFYESSPQVLHTEVLOHLTDLIRNHPWS 120
QY    121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRGDGEILVELVOYCHTQMD 180
DB    121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRGDGEILVELVOYCHTQMD 180
QY    181 VTDYKGETVFHYAVOGDNSQVLQLLRNAVAGLNQNNQGLTPHLACQLGKQEMVRVLL 240
DB    181 VTDYKGETVFHYAVOGDNSQVLQLLRNAVAGLNQNNQGLTPHLACQLGKQEMVRVLL 240
QY    241 LCNARCNIMGPNPYTHSAKFSGKGCAMIIISMDSOIHSKDPRYGASPLHWAKNAEMA 300
DB    241 LCNARCNIMGPNPYTHSAKFSGKGCAMIIISMDSOIHSKDPRYGASPLHWAKNAEMA 300
QY    301 RMLLKRCGNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGNTPLHLAMSK 360
DB    301 RMLLKRCGNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGNTPLHLAMSK 360
QY    361 DNVEMIKALIVFGAEVDTNPDFGTPTFLASKIG 394
DB    361 DNVEMIKALIVFGAEVDTNPDFGTPTFLASKIG 394

RESULT 4
US-09-927-180-2
; Sequence 2, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
;   Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: 09/519,223

; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
;   NAME: Brown, Scott A.
;   TELEPHONE: (617) 498-8224
;   TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 688 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-927-180-23

Query Match      100.0%; Score 2084; DB 9; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.1e-130;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY    1 MQFFGLVNTFSGVNLFNSNPFRVKEAVADYTSSDRVRREGQLILFQNTPNRTWDCVLV 60
DB    1 MQFFGRLVNTLSSVTNLFSNPFRVKEISVDYTSHERVREBQQLILFQNASRNTWDCLV 60
QY    61 NPNRSOSGRFLFOLEADALVNPHOYSSQLLPFYESSPQVLHTEVLOHLTDLIRNHPWS 120
DB    61 NPNRSOSGRFLFOLEADALVNPHOYSSQLLPFYESSPQVLHTEVLOHLTDLIRNHPWS 120
QY    121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRGDGEILVELVOYCHTQMD 180
DB    121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRGDGEILVELVOYCHTQMD 180
QY    181 VTDYKGETVFHYAVOGDNSQVLQLLRNAVAGLNQNNQGLTPHLACQLGKQEMVRVLL 240
DB    181 VTDYKGETVFHYAVOGDNSQVLQLLRNAVAGLNQNNQGLTPHLACQLGKQEMVRVLL 240
QY    241 LCNARCNIMGPNPYTHSAKFSGKGCAMIIISMDSOIHSKDPRYGASPLHWAKNAEMA 300
DB    241 LCNARCNIMGPNPYTHSAKFSGKGCAMIIISMDSOIHSKDPRYGASPLHWAKNAEMA 300
QY    301 RMLLKRCGNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGNTPLHLAMSK 360
DB    301 RMLLKRCGNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGNTPLHLAMSK 360
QY    361 DNVEMIKALIVFGAEVDTNPDFGTPTFLASKIG 394
DB    361 DNVEMIKALIVFGAEVDTNPDFGTPTFLASKIG 394

RESULT 5
US-10-108-260A-3778
; Sequence 3778, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3778
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3778

Query Match      59.2%; Score 1234.5; DB 15; Length 667;
Best Local Similarity 64.0%; Pred. No. 3.2e-109;
Matches 252; Conservative 1; Mismatches 2; Indels 139; Gaps 1;

QY    1 MQFFGRLVNTFSGVNLFNSNPFRVKEAVADYTSSDRVRREGQLILFQNTPNRTWDCVLV 60

```

LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-927-180-17

Query Match 100.0%; Score 2084; DB 9; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-191;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTNLFNSNPRVKEVAVADYSSDRVREEGQLILFQNTNRTWDCVLV 60
DB 1 MOFFGRLVNTFSGVTNLFNSNPRVKEVAVADYSSDRVREEGQLILFQNTNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLEADALVNFHQSOLLPPFYESSQVLTHTVQLHTLTLIRNHPW 120
DB 61 NPNRSQSGFRLFQLEADALVNFHQSOLLPPFYESSQVLTHTVQLHTLTLIRNHPW 120
QY 121 SVAHLAVELGIRECFPHHSRIISCANCAENEGCTPLHLACRGDGEIIVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFPHHSRIISCANCAENEGCTPLHLACRGDGEIIVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRCGNVNTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCGNVNTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDPGETPTFLASKIG 394
DB 361 DNVEIMKALIVFGAEVDTNDPGETPTFLASKIG 394

RESULT 2
US-09-927-180-21
; Sequence 21, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match 100.0%; Score 2084; DB 9; Length 687;
Best Local Similarity 100.0%; Pred. No. 1.1e-190;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTNLFNSNPRVKEVAVADYSSDRVREEGQLILFQNTNRTWDCVLV 60
DB 1 MOFFGRLVNTFSGVTNLFNSNPRVKEVAVADYSSDRVREEGQLILFQNTNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLEADALVNFHQSOLLPPFYESSQVLTHTVQLHTLTLIRNHPW 120
DB 61 NPNRSQSGFRLFQLEADALVNFHQSOLLPPFYESSQVLTHTVQLHTLTLIRNHPW 120
QY 121 SVAHLAVELGIRECFPHHSRIISCANCAENEGCTPLHLACRGDGEIIVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFPHHSRIISCANCAENEGCTPLHLACRGDGEIIVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRCGNVNTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCGNVNTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDPGETPTFLASKIG 394
DB 361 DNVEIMKALIVFGAEVDTNDPGETPTFLASKIG 394

RESULT 3
US-09-927-180-23
; Sequence 23, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:20:02 ; Search time 53.7186 Seconds
(without alignments)
2530.207 Million cell updates/sec

Title: US-10-612-668-17

Perfect score: 2084

Sequence: 1 MGFRLVNTSGVTNLFSEN.....EVDTPNDFGTFFLASKIG 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 1462099

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2084	100.0	687	9	US-09-927-180-21
3	2084	100.0	688	9	US-09-927-180-23
4	1837	88.1	752	9	US-09-927-180-2
5	1234.5	59.2	667	15	US-10-108-260A-3778
6	324	15.5	1330	15	US-10-108-260A-3237
7	301	14.4	786	14	US-10-164-080-2
8	301	14.4	786	14	US-10-299-327-2
9	301	14.4	786	14	US-10-128-174-13
10	301	14.4	786	14	US-10-128-174-31
11	301	14.4	786	14	US-10-128-174-32
12	301	14.4	786	14	US-10-128-174-33
13	301	14.4	787	10	US-09-866-050A-334

14	300.5	14.4	347	14	US-10-128-174-30	Sequence 30, Appl
15	300.5	14.4	1724	9	US-09-964-899-43	Sequence 43, Appl
16	296	14.2	1094	17	US-10-479-764-22	Sequence 22, Appl
17	296	14.2	3913	15	US-10-334-143-45	Sequence 45, Appl
18	288	13.8	1762	14	US-10-205-194-117	Sequence 117, Appl
19	283.5	13.6	784	14	US-10-164-080-7	Sequence 7, Appl
20	283.5	13.6	784	15	US-10-258-951-70	Sequence 70, Appl
21	281.5	13.5	784	14	US-10-354-358-38	Sequence 38, Appl
22	281.5	13.5	784	14	US-10-128-174-12	Sequence 12, Appl
23	281.5	13.5	784	15	US-10-658-904-2	Sequence 2, Appl
24	280.5	13.5	720	15	US-10-433-794-20	Sequence 20, Appl
25	280.5	13.5	765	14	US-10-128-174-3	Sequence 3, Appl
26	280.5	13.5	765	14	US-10-128-174-34	Sequence 34, Appl
27	280.5	13.5	765	14	US-10-128-174-35	Sequence 35, Appl
28	280.5	13.5	765	14	US-10-128-174-36	Sequence 36, Appl
29	280.5	13.5	765	14	US-10-128-174-37	Sequence 37, Appl
30	280.5	13.5	765	14	US-10-128-174-38	Sequence 38, Appl
31	280.5	13.5	765	14	US-10-128-174-39	Sequence 39, Appl
32	280.5	13.5	765	14	US-10-128-174-40	Sequence 40, Appl
33	280.5	13.5	765	14	US-10-128-174-41	Sequence 41, Appl
34	280.5	13.5	765	14	US-10-128-174-42	Sequence 42, Appl
35	280.5	13.5	765	14	US-10-128-174-43	Sequence 43, Appl
36	280.5	13.5	765	14	US-10-128-174-44	Sequence 44, Appl
37	280.5	13.5	765	15	US-10-182-243-56	Sequence 56, Appl
38	278.5	13.4	784	16	US-10-648-593-153	Sequence 153, Appl
39	272	13.1	367	15	US-10-250-613-6	Sequence 6, Appl
40	272	13.1	994	17	US-10-717-665-38	Sequence 38, Appl
41	272	13.1	1056	17	US-10-479-764-18	Sequence 18, Appl
42	271.5	13.0	1053	15	US-10-291-172-343	Sequence 343, Appl
43	271.5	13.0	1053	15	US-10-221-278-343	Sequence 343, Appl
44	267.5	12.8	919	15	US-10-108-260A-4122	Sequence 4122, Ap
45	258	12.4	1023	15	US-10-369-493-6689	Sequence 6689, Ap

ALIGNMENTS

RESULT 1

US-09-927-180-17
; Sequence 17, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
;

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Search completed: May 26, 2005, 14:13:49
Job time : 60.101 secs

PI Tang J, Jones S;
XX WPI; 1997-076789/07.
DR N-PSDB; AAT59199.
XX
XX
PT Compan. comprising calcium-independent phospholipase enzyme - for
PT screening for anti-inflammatory agents.
XX
PS Claim 5; Col 15-22; 24pp; English.
XX
CC This is the amino acid sequence of the Ca-independent phospholipase A2/B
CC from Chinese hamster ovary cells. The protein was isolated from these
CC cells by conventional chromatographic methods e.g. DEAE anion exchange,
CC hydrophobic interaction, heparin Toyopearl and Mono P 5/20
CC chromatofocusing chromatography. The purified protein has mol. wt. of 86
CC kD and an optimum pH 6. The protein was used for amino acid sequencing
CC from which pools of degenerate probes were synthesised. The probes were
CC used to screen a CHO cell cDNA library in lambda ZAPII vector. Of 40000
CC recombinant phages screened, 12 positive plaques were isolated. One of
CC these, designated clone 9, contained this sequence. The phospholipase
CC gene can be inserted into eukaryotic vectors for expression in COS or CHO
CC cells. The protein, or peptides derived from it e.g. AAW13164-76, can be
CC used to identify phospholipase inhibitors that can be used as anti-
CC inflammatory agents, esp. against components of the arachidonic acid
CC cascade. (Updated on 25-WAR-2003 to correct PF field.) (Updated on 17-OCT
CC -2003 to standardise OS field)
XX
SQ Sequence 752 AA;

Query Match 88.1%; Score 1837; DB 2; Length 752;
Best Local Similarity 87.3%; Pred. No. 1.1e-191;
Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 MQFFGRLVNTSGVTNLFNSNPRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGRLVNTLSSVTNLFNSNPRVKEISVADYTSHERVREEGQLILFQNASNRTWDCILV 60

QY 61 NPNRSQSGFRLFQLEADALVNFHQSQQLPFYESSQVLTHTVQLHQLTLIRNHPSW 120
Db 61 SPRNPHSGFRLFQLESEADALVNFQFSSQLPFYESSQVLTHTVQLHQLTLIRNHPSW 120

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Db 181 VTDNKGETAHYAVQGDNSQVLQLGKNASAGLNQVNNQGLTPLHLACQMGQEMVRVLL 240

QY 241 LCNARCNIMGNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNVMGSPGFPHTAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300

QY 301 RMLLRGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLRGCNDVSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360

QY 361 DNMEMIKALIVFGAEVDTNDPGETPTFLASKI 393
Db 361 DNMEMIKALIVFGAEVDTNDPGETPTAFWASKI 393

RESULT 15
ID AAW17849
XX AAW17849 standard; protein; 752 AA.
AC AAW17849;
XX
XX 27-AUG-2003 (revised)
DT 07-AUG-1997 (first entry)
XX
DE Hamster cytosolic phospholipase A2/B.
XX

KW Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
KW inflammation; inhibitor; antiinflammatory; CHO.
XX
OS Cricetus.
FH Key Location/Qualifiers
FT Active-site 465
FT /note= "mutagenesis of Ser-465 results in loss of
FT activity"
XX
PN WO9717448-A2.
XX
XX 15-MAY-1997.
XX
PF 07-NOV-1996; 96WO-US017794.
XX
PR 08-NOV-1995; 95US-00555568.
XX (GENY) GENETICS INST INC.
XX
XX Jones S, Tang J;
PI WPI; 1997-281037/25.
DR N-PSDB; AAT68827.
XX
XX Calcium independent phospholipase A2/B - used to reduce inflammation in a
PT mammalian subject.
PT
XX
PS Example 4; Page 33-36; 74pp; English.
XX
CC A novel hamster cytosolic phospholipase A2/B (sPLA2/B) (AAW17849) is
CC thought to be involved in the arachidonic acid cascade. Its amino acid
CC sequence was deduced from a cDNA clone (AAT68827) obtd. from a CHO-DUX
CC cDNA library. The recombinant enzyme has been expressed in CHO and COS
CC host cells. Human sPLA2/B polypeptides (see also AAW17845-48) have also
CC been isolated. These can be used to screen for inhibitors useful as
CC antiinflammatory agents that block the arachidonic acid cascade in
XX mammals. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 752 AA;

Query Match 88.1%; Score 1837; DB 2; Length 752;
Best Local Similarity 87.3%; Pred. No. 1.1e-191;
Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 MQFFGRLVNTSGVTNLFNSNPRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGRLVNTLSSVTNLFNSNPRVKEISVADYTSHERVREEGQLILFQNASNRTWDCILV 60

QY 61 NPNRSQSGFRLFQLEADALVNFHQSQQLPFYESSQVLTHTVQLHQLTLIRNHPSW 120
Db 61 SPRNPHSGFRLFQLESEADALVNFQFSSQLPFYESSQVLTHTVQLHQLTLIRNHPSW 120

QY 121 SVHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRGDGEILVELVOYCHTOMD 180
Db 121 VTDLKGETAFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQMGQEMVRVLL 240

QY 181 VTDNKGETAHYAVQGDNSQVLQLGKNASAGLNQVNNQGLTPLHLACQMGQEMVRVLL 240
Db 181 VTDNKGETAHYAVQGDNSQVLQLGKNASAGLNQVNNQGLTPLHLACQMGQEMVRVLL 240

QY 241 LCNARCNIMGNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNVMGSPGFPHTAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300

QY 301 RMLLRGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLRGCNDVSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360

QY 361 DNMEMIKALIVFGAEVDTNDPGETPTFLASKI 393
Db 361 DNMEMIKALIVFGAEVDTNDPGETPTAFWASKI 393

Best Local Similarity 87.3%; Pred. No. 1.1e-191;
Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSQVTLNFSNPRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
DB 1 MOFFGRLVNTLSVTLNFSNPRVKEISVADYTSHERVREEGQLILFQNASNRTWDCILV 60
QY 61 NPNRSQSGFRLFOLELEADALVNFHQYSQQLPFFYESSQVLHTEVLOHLTDLIRNHPWS 120
DB 61 SPNPHSGFRLFOLESEADALVNFQFSSQLPFFYESSQVLHVEVLQHLSDLIRSHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDSGILVELVOYCHTQMD 180
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEEGCTPLHLACRKGDSILVELVOYCHAQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQILGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDNKGETAFAHYAVQGDNSQVLQILGNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAKFSSQKCAEMIISMDSQIHSKDPKYGASPLHWAKNAEMA 300
DB 241 LCNARCNVMGSPGFPIHTAMKFSQKCAEMIISMDSQIHSKDPKYGASPLHWAKNAEMA 300
QY 301 RMLLKRGCVNNTSSAGNTALHVGVMNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRGCDVDSTSAAGNTALHVAVMNRNRFDCVMVLLTYGANAGTPEHGNTPLHLAISK 360
QY 361 DNMEMIKALIVFGAEVDTNDFGETPFLASKI 393
DB 361 DNMEMIKALIVFGAEVDTNDFGETPAPFASKI 393

RESULT 13
AAW01479
ID AAW01479 standard; protein; 752 AA.
XX
AC AAW01479;
XX
DT 25-MAR-2003 (revised)
DT 12-FEB-1997 (first entry)
XX
DE Calcium-independent cytosolic phospholipase A2/B.
XX
KW cPLA2/B; calcium-independent cytosolic phospholipase A2/B;
KW arachidonic acid; 1-palmitoyl-2-[14C]-arachidonyl-phosphatidylcholine;
KW anti-inflammatory; screen; rheumatoid arthritis.
XX
OS Synthetic.
XX
PN US5554511-A.
XX
PD 10-SEP-1996.
XX
PF 14-APR-1995; 95US-00422420.
XX
PR 27-JUL-1994; 94US-00281193.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Tang J, Jones S;
XX
DR WPI; 1996-424653/42.
DR N-PSDB; AAT44578.
XX
PT Prodn. of a Ca-independent cytosolic phospholipase A(2)/B - by culturing
PT host cells contg. the phospholipase gene, useful for screening anti-
PT inflammatory agents for treating e.g. rheumatoid arthritis.
XX
PS Claim 1; Col 15-22; 24pp; English.
XX
CC The present sequence is that of a calcium-independent cytosolic
CC phospholipase A2/B (cPLA2/B) enzyme. cPLA2/B is important in the release
CC of arachidonic acid in specific tissues characterised by unique membrane

phospholipids. The invention provides a process for producing such an enzyme. The enzyme has a mol. wt. of 86 kD on SDS-PAGE and the presence of one or more amino acid sequences selected from AAW01480-92. cPLA2/B has activity in a mixed micelle assay with 1-palmitoyl-2-[14C]-arachidonyl-phosphatidylcholine. The enzyme is useful for screening anti-inflammatory agents mediated by the arachidonic acid cascade, for treating, e.g. rheumatoid arthritis (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 752 AA;
SQ

Query Match 88.1%; Score 1837; DB 2; Length 752;
Best Local Similarity 87.3%; Pred. No. 1.1e-191;
Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSQVTLNFSNPRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
DB 1 MOFFGRLVNTLSVTLNFSNPRVKEISVADYTSHERVREEGQLILFQNASNRTWDCILV 60
QY 61 NPNRSQSGFRLFOLELEADALVNFHQYSQQLPFFYESSQVLHTEVLOHLTDLIRNHPWS 120
DB 61 SPNPHSGFRLFOLESEADALVNFQFSSQLPFFYESSQVLHVEVLQHLSDLIRSHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDSGILVELVOYCHTQMD 180
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEEGCTPLHLACRKGDSILVELVOYCHAQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQILGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDNKGETAFAHYAVQGDNSQVLQILGNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAKFSSQKCAEMIISMDSQIHSKDPKYGASPLHWAKNAEMA 300
DB 241 LCNARCNVMGSPGFPIHTAMKFSQKCAEMIISMDSQIHSKDPKYGASPLHWAKNAEMA 300
QY 301 RMLLKRGCVNNTSSAGNTALHVGVMNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRGCDVDSTSAAGNTALHVAVMNRNRFDCVMVLLTYGANAGTPEHGNTPLHLAISK 360
QY 361 DNMEMIKALIVFGAEVDTNDFGETPFLASKI 393
DB 361 DNMEMIKALIVFGAEVDTNDFGETPAPFASKI 393

RESULT 14
AAW13163
ID AAW13163 standard; protein; 752 AA.
XX
AC AAW13163;
XX
DT 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 20-MAY-1997 (first entry)
XX
DE Ca-independent phospholipase A2/B protein.
XX
KW Ca-independent phospholipase A2/B; Chinese hamster ovary cell; probe;
KW chromatography; DEAE anion exchange; hydrophobic interaction; lambda;
KW heparin Toyopearl; chromatofocussing; eukaryotic expression vector; COS;
KW CHO; inhibitor; anti-inflammatory agent; arachidonic acid cascade.
OS Cricetulus griseus; ovary cells.
XX
PN US5589170-A.
XX
PD 31-DEC-1996.
XX
PF 14-APR-1995; 95US-00422106.
XX
PR 27-JUL-1994; 94US-00281193.
XX
PA (GEMY) GENETICS INST INC.
XX

AC ABM84354;
 DT 18-NOV-2004 (first entry)
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4603.
 KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
 XX Homo sapiens.
 OS WO2004023973-A2.
 PN 25-MAR-2004.
 PD 12-SEP-2003; 2003WO-US028227.
 XX 12-SEP-2002; 2002US-04102599.
 PR 12-SEP-2002; 2002US-04102609.
 XX (INCY-) INCYTE CORP.
 PA Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 PI Harthshorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV;
 PI Mooney EM, Deleane AM, Panesar IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patuary S, Shi X, Suarez CJ;
 XX WPI: 2004-329368/30.
 DR N-PSDB; ACM43006.
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX Claim 27; Page; 190pp; English.
 PS The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorders, developmental disorders, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX Sequence 810 AA;
 SQ
 Query Match 98.6%; Score 2054; DB 8; Length 810;
 Best Local Similarity 93.1%; Pred. No. 1.7e-215;
 Matches 393; Conservative 0; Mismatches 1; Indels 28; Gaps 1;
 QY 1 MOFFGRLVNTFGVNTLFSNPRVRKEVAVADYTSSDRVREGLILFQNTPNRTWDCVLV 60
 DB 1 MOFFGRLVNTFGVNTLFSNPRVRKEVAVADYTSSDRVREGLILFQNTPNRTWDCVLV 60
 QY 61 NPNRSQSGFRLQLLEADALVNFHOYSQQLLPFFYESPQVLHTEVQLHTDLIRNPSW 120
 DB 61 NPNRSQSGFRLQLLEADALVNFHOYSQQLLPFFYESPQVLHTEVQLHTDLIRNPSW 120
 QY 121 SVAHLAVELGIRECFHHSRII-----SCANCAENREG 152
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DB 121 SVAHLAVELGIRECFHHSRIIRVRSAHQVPGVLWELISTHHEIFSPQPPXSCANCAENREG 180
 QY 153 CTPLHLACRKGDEILVELVOYCHTQMDVTDYKGETVFHYAVQGDNSQVQLLGRNAVAG 212
 DB 181 CTPLHLACRKGDEILVELVOYCHTQMDVTDYKGETVFHYAVQGDNSQVQLLGRNAVAG 240
 QY 213 LNOVNNQGLTPLHLACQLGQEMVRVLLCNARCINMGPNGYPIHSAMKFSQKCAEMII 272
 DB 241 LNOVNNQGLTPLHLACQLGQEMVRVLLCNARCINMGPNGYPIHSAMKFSQKCAEMII 300
 QY 273 SMDSSQIHSKDPYRGASPLHWAKNAEMARMLLKRCNVNSTSSAGNTALHVGVMNRNEDC 332
 DB 301 SMDSSQIHSKDPYRGASPLHWAKNAEMARMLLKRCNVNSTSSAGNTALHVGVMNRNEDC 360
 QY 333 AIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTPNDFGTPPTFLASK 392
 DB 361 AIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTPNDFGTPPTFLASK 420
 QY 393 IG 394
 DB 421 IG 422
 RESULT 12
 AAR83018
 ID AAR83018 standard; protein; 752 AA.
 AC AAR83018;
 XX 15-JUN-1996 (first entry)
 DT Calcium-independent cytosolic phospholipase-A2/B enzyme.
 DE CHO; calcium-independent cytosolic phospholipase-A2/B; enzyme;
 KW phospholipase-A2; phospholipase-B; drug screening; antiinflammatory;
 KW antibody.
 XX Cricetulus griseus.
 OS US5466595-A.
 PN 14-NOV-1995.
 PD 27-JUL-1994; 94US-00281193.
 PF 27-JUL-1994; 94US-00281193.
 PR (GEMY) GENETICS INST INC.
 PA Tang J, Jones S;
 PI WPI; 1996-009526/01.
 DR N-PSDB; AAT05842.
 XX Isolated polynucleotide encoding cytosolic phospholipase A2/8 - for
 PT producing enzyme for use in screening anti-inflammatory agents and prodn.
 PT of antibodies.
 PS Claim 5; Col 15-22; 24pp; English.
 CC The enzyme may be produced recombinantly in host cells such as animal
 CC cells, insect cells, eukaryotes, prokaryotes, etc. The protein may also
 CC be expressed in transgenic animals (e.g. milk of transgenic cow). The
 CC protein is used to screen for agents which inhibit phospholipase activity
 CC for use as antiinflammatory agents. These agents can be used to treat
 CC e.g. rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease
 CC and other disease mediated by increased levels of prostaglandins,
 CC leukotriene or platelet activating factor. The enzyme can also be used
 CC for the production of antibodies for use as research or diagnostic tools
 SQ Sequence 752 AA;
 Query Match 88.1%; Score 1837; DB 2; Length 752;

CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating diseases of the
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polypeptide of the
CC invention.
XX
SQ Sequence 806 AA;

Query Match 99.7%; Score 2078; DB 8; Length 806;
Best Local Similarity 99.7%; Pred. No. 4e-218; 1; Indels 0; Gaps 0;
Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTNLFNPNPRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MOFFGRLVNTFSGVTNLFNPNPRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60

QY 61 NPRNSQSGFRLFQLELEADALVNFHQSOLLPPFYESSQVLHTEVLQHLTDLIRNHPSW 120
DB 61 NPRNSQSGFRLFQLELEADALVNFHQSOLLPPFYESSQVLHTEVLQHLTDLIRNHPSW 120

QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240

QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300

QY 301 RMLLRKGCNVNSTSAGNTALHVGWNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRKGCNVNSTSAGNTALHVGWNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360

QY 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394

RESULT 10
ABM84355
ID ABM84355 standard; protein; 810 AA.
XX
AC ABM84355;
XX
DT 18-NOV-2004 (first entry)
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4604.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
FN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney BW, Deleage AM, Panesar IS, Banville SC, Reddy IP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI: 2004-329368/30.
DR N-PSDB; ACN43007.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 810 AA;

Query Match 98.6%; Score 2054; DB 8; Length 810;
Best Local Similarity 93.1%; Pred. No. 1.7e-215; 1; Indels 28; Gaps 1;
Matches 393; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MOFFGRLVNTFSGVTNLFNPNPRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MOFFGRLVNTFSGVTNLFNPNPRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60

QY 61 NPRNSQSGFRLFQLELEADALVNFHQSOLLPPFYESSQVLHTEVLQHLTDLIRNHPSW 120
DB 61 NPRNSQSGFRLFQLELEADALVNFHQSOLLPPFYESSQVLHTEVLQHLTDLIRNHPSW 120

QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 152
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 152

QY 153 CTPLHLACRKGDEILVELVQYCHTQMDVTDYKGETVFHYAVQGDNSQVLQLGRNAVAG 212
DB 181 CTPLHLACRKGDEILVELVQYCHTQMDVTDYKGETVFHYAVQGDNSQVLQLGRNAVAG 240

QY 213 LNQVNNQGLTPLHLACOLGKQEMVRVLLCNARCNIMGPNGYPIHSAMKFSQKCAEMII 272
DB 241 LNQVNNQGLTPLHLACOLGKQEMVRVLLCNARCNIMGPNGYPIHSAMKFSQKCAEMII 300

QY 273 SMDSSQIHSKDPYRGASPLHWAKNAEMARMLLKRCNVNSTSAGNTALHVGWNRNRPD 332
DB 301 SMDSSQIHSKDPYRGASPLHWAKNAEMARMLLKRCNVNSTSAGNTALHVGWNRNRPD 360

QY 333 AIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTNDGFTPTFLASK 392
DB 361 AIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTNDGFTPTFLASK 420

QY 393 IG 394
DB 421 IG 422

RESULT 11
ABM84354
ID ABM84354 standard; protein; 810 AA.
XX

PS	Claim 6; Page 28-30; 4lpp; English.	
XX	The invention relates to a purified mammalian calcium independent	
CC	cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is	
CC	characterized by activity in the absence of calcium and has a molecular	
CC	weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified	
CC	calcium independent phospholipase enzyme is useful for identifying an	
CC	inhibitor of phospholipase activity which involves combining (I),	
CC	phospholipid and candidate inhibitor compound, and observing whether the	
CC	enzyme cleaves the phospholipid and releases fatty acid from it. A	
CC	pharmaceutical composition (PC) comprising a therapeutically effective	
CC	amount of the inhibitor is useful for reducing inflammation and for	
CC	treating inflammatory conditions including rheumatoid arthritis,	
CC	psoriasis, asthma, inflammatory bowel disease and other diseases mediated	
CC	by increased levels of prostaglandins, leukotriene or platelet activating	
CC	factor. A composition comprising an antibody which binds to (I) is useful	
CC	as research and diagnostic tool, and is also useful in the study of	
CC	phospholipase A2 activity and inflammatory conditions. The present	
CC	sequence represents a human cPLA2/B enzyme longer splice variant (clone	
CC	19b)	
XX	Sequence 688 AA;	
SQ	Query Match 100.0%; Score 2084; DB 5; Length 688;	
	Best Local Similarity 100.0%; Pred. No. 6.8e-219;	
	Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MOFFGRLVNTFSGVTNLFNSNPRFRKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60	
DB	1 MOFFGRLVNTFSGVTNLFNSNPRFRKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60	
QY	61 NPNRSQSGFRLPQLELEADALVNFHQSQVLLPFYESSQVLTHTVQLHTDLIRNHPWS 120	
DB	61 NPNRSQSGFRLPQLELEADALVNFHQSQVLLPFYESSQVLTHTVQLHTDLIRNHPWS 120	
QY	121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDDGELLVELVQYCHTQMD 180	
DB	121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDDGELLVELVQYCHTQMD 180	
QY	181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLVNQQGLTPLHLACQLGQEMVRVLL 240	
DB	181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLVNQQGLTPLHLACQLGQEMVRVLL 240	
QY	241 LCNARCINMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300	
DB	241 LCNARCINMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300	
QY	301 RMLLKRGCVNSTSSAGNTALHVGVMNRNRFDCAI VLLTHGANADARGEHGNTPHLAMSK 360	
DB	301 RMLLKRGCVNSTSSAGNTALHVGVMNRNRFDCAI VLLTHGANADARGEHGNTPHLAMSK 360	
QY	361 DNVEIMKALIVFGAEVDTNDGFTPTFLASKIG 394	
DB	361 DNVEIMKALIVFGAEVDTNDGFTPTFLASKIG 394	
RESULT 7		
ADD93407	standard; protein; 784 AA.	
ID	ADD93407	
XX	ADD93407;	
AC	ADD93407;	
XX	ADD93407;	
DT	29-JAN-2004 (first entry)	
XX	Human lipid-associated molecule LIPAM-14 polypeptide.	
DE	Human; lipid-associated molecule; LIPAM-14; neuroprotective; relaxant;	
KW	antithyroid; antidiabetic; cytostatic; dermatological; immunosuppressive;	
KW	antiinflammatory; thymomimetic; antiallergic; cerebroprotective;	
KW	gastrointestinal; hepatotropic; nephrotropic; anticonvulsant;	
KW	antiparkinsonian; antibacterial; antiparasitic; fungicide; protozoacide;	
KW	virucide; uropathic; antirheumatic; cardiant; cardiovascular; anti-HIV;	
KW	nootropic.	
XX		
OS	Homo sapiens.	
XX	WO2003083081-A2.	
PN	09-OCT-2003.	
PD	27-MAR-2003; 2003WO-US0009755.	
XX	29-MAR-2002; 2002US-0368722P.	
PR	03-MAY-2002; 2002US-0377576P.	
PR	05-JUL-2002; 2002US-0393934P.	
PR	27-SEP-2002; 2002US-0414269P.	
XX	(INCY-) INCYTE CORP.	
PA	Emerling BM, Marquis JP, Chawla NK, Lee SY, Duggan BM, Warren BA;	
PI	Baughn MR, Lee EA, Griffin JA, Kabie AE, Elliott VS, Chang H;	
PI	Lee S, Rankumar J, Bulloch SA, Hafalia AJA, Khare R, Jiang X;	
PI	Jackson AA;	
XX	WPI; 2003-788347/74.	
DR	N-PSDB; ADD93426.	
XX	New LIPAM polypeptides, useful for diagnosing, preventing, and treating	
PT	disorders associated with abnormal expression or activity of LIPAM, e.g.	
PT	neuromuscular, immunological, cardiovascular disorders, cancer and/or	
PT	infections.	
XX	Claim 69; Page 206-207; 238pp; English.	
PS	The present sequence is the protein sequence of human lipid-associated	
XX	molecule LIPAM-14 (Incyte polypeptide 7512662CD1), a protein that shows	
CC	homology to human Ca ²⁺ -independent phospholipase A2 short isoform. This	
CC	is one of 19 LIPAM polypeptides of the invention. The invention relates	
CC	to these novel LIPAMs and the nucleic acids encoding them, and to the use	
CC	of nucleic acids and proteins in the diagnosis, treatment and prevention	
CC	of disorders associated with abnormal expression or activity of LIPAM	
CC	such as neurodegenerative disorders (e.g. Parkinson's disease,	
CC	Alzheimer's disease), muscular disorders (e.g. myotonic dystrophy,	
CC	catatonnia), endocrine disorders (e.g. diabetes, Grave's disease), cancers	
CC	(e.g. leukemia, cervical or breast cancers), immunological disorders	
CC	(e.g. scleroderma, systemic lupus erythematosus, allergies),	
CC	gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g.	
CC	Goodpasture's syndrome), infections (e.g. viral, bacterial, fungal,	
CC	parasitic, protozoal, helminthic), cardiovascular disorders (e.g.	
CC	atherosclerosis), or hepatic diseases (e.g. cirrhosis). The invention	
CC	also relates to the assessment of the effects of exogenous compounds on	
CC	the expression of nucleic acids and LIPAMs. The invention provides	
CC	expression vectors, host cells, antibodies, agonists and antagonists,	
CC	transgenic organisms, and arrays and microarrays of the polynucleotides.	
XX	Sequence 784 AA;	
SQ	Query Match 99.7%; Score 2078; DB 7; Length 784;	
	Best Local Similarity 99.7%; Pred. No. 3.8e-218;	
	Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 MOFFGRLVNTFSGVTNLFNSNPRFRKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60	
DB	33 MOFFGRLVNTFSGVTNLFNSNPRFRKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 92	
QY	61 NPNRSQSGFRLPQLELEADALVNFHQSQVLLPFYESSQVLTHTVQLHTDLIRNHPWS 120	
DB	93 NPNRSQSGFRLPQLELEADALVNFHQSQVLLPFYESSQVLTHTVQLHTDLIRNHPWS 152	
QY	121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDDGELLVELVQYCHTQMD 180	
DB	153 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDDGELLVELVQYCHTQMD 212	
QY	181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLVNQQGLTPLHLACQLGQEMVRVLL 240	
DB	213 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLVNQQGLTPLHLACQLGQEMVRVLL 272	

QY 121 SVAHLAVELGIRECFHSHSRIISCANCAENEECTPLHLACRKGDEGILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHSHSRIISCANCAENEECTPLHLACRKGDEGILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNPGYPIHSAKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNPGYPIHSAKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRGCNVNSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHGNTPHLHMSK 360
DB 301 RMLLRGCNVNSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHGNTPHLHMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394

RESULT 5
AAW17848
ID AAW17848 standard; protein; 688 AA.
AC AAW17848;
XX

DT 07-AUG-1997 (first entry)
XX Cytosolic phospholipase A2/B (alternatively spliced clone 19b).
DE Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
KW inflammation; inhibitor; antiinflammatory.
XX

OS Homo sapiens.
XX
PN WO9717448-A2.
XX
PD 15-MAY-1997.
XX

PF 07-NOV-1996; 96WO-US017794.
XX
XX 08-NOV-1995; 95US-00555568.
XX

PA (GEMY) GENETICS INST INC.
XX

PI Jones S, Tang J;
XX
DR WPI: 1997-281037/25.
XX
DR N-PSDB; AAT68826.
XX

XX Calcium independent phospholipase A2/B - used to reduce inflammation in a
PT mammalian subject.
XX

PS Claim 12; Page 54-56; 74pp; English.
XX

XX A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17848) is
CC characterised by activity in the absence of calcium, by activity in a
CC mixed micelle assay with 1-palmitoyl-2-(14C)- arachidonyl-
CC phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a
CC lack of stimulation by ATP, and by including in its sequence at least one
CC of the amino acid sequences given in AAW17839- 44). It is an
CC alternatively spliced variant of another isolated polypeptide (AAW17846)
CC and is encoded by an isolated cDNA (AAT68826). Other PLA2/B enzymes
CC (AAW17845, AAW17847) have also been identified. sPLA2/B enzymes are
CC thought to be involved in the release of arachidonic acid in specific
CC tissues. Recombinant sPLA2/B polypeptides produced in transformed host
CC cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory
CC drugs which inhibit the arachidonic acid cascade
XX

SQ Sequence 688 AA;
XX

Query Match 100.0%; Score 2084; DB 2; Length 688;
XX

Best Local Similarity 100.0%; Pred. No. 6.8e-219;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MOFFGRLVNTSGVNTLFSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLL 60
DB 1 MOFFGRLVNTSGVNTLFSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLL 60
QY 61 NPNRSQSGFRLLFQLEADALVNFHQYSSQLLPFYESSQVLTHTVLOHLDLIRNHPSW 120
DB 61 NPNRSQSGFRLLFQLEADALVNFHQYSSQLLPFYESSQVLTHTVLOHLDLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHSHSRIISCANCAENEECTPLHLACRKGDEGILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHSHSRIISCANCAENEECTPLHLACRKGDEGILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNPGYPIHSAKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNPGYPIHSAKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRGCNVNSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHGNTPHLHMSK 360
DB 301 RMLLRGCNVNSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHGNTPHLHMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394

RESULT 6
ABB82232

ID ABB82232 standard; protein; 688 AA.
XX

AC ABB82232;
XX

DT 08-JAN-2003 (first entry)
XX

DE Human cPLA2/B splice variant (clone 19b).
XX

KW Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
KW antiinflammatory; antiarthritic; antipsooriatic; antirheumatic; cytosolic;
KW antiasthmatic; human.
XX

OS Homo sapiens.
XX

PN US2002106364-A1.
XX

PD 08-AUG-2002.
XX

PF 09-AUG-2001; 2001US-00927180.
XX

PR 27-JUL-1994; 94US-00281193.
XX

PR 14-APR-1995; 95US-00422106.
XX

PR 14-APR-1995; 95US-00422420.
XX

PR 26-JUN-1995; 95WO-US008069.
XX

PR 08-NOV-1995; 95US-00555568.
XX

PR 09-SEP-1998; 98US-00149988.
XX

PR 06-MAR-2000; 2000US-00519223.
XX

PA (GEMY) GENETICS INST INC.
XX

PI Jones S, Tang J;
XX

XX WPI; 2002-73923/80.
XX

DR N-PSDB; ABV73011.
XX

XX Novel composition comprising purified mammalian calcium independent
PT phospholipase enzyme, useful for the screening of inhibitors of
PT phospholipase activity, is active in the absence of calcium.
XX

XX WO9717448-A2.
 XX 15-MAY-1997.
 XX 07-NOV-1996; 96WO-US017794.
 XX 08-NOV-1995; 95US-00555568.
 XX (GEMY) GENETICS INST INC.
 XX Jones S, Tang J;
 XX WPI; 1997-281037/25.
 XX N-PSDB; AAT68825.
 XX Calcium independent phospholipase A2/B - used to reduce inflammation in a
 PT mammalian subject.
 XX Claim 12; Page 49-51; 74pp; English.
 XX A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17847) is
 CC characterised by activity in the absence of calcium, by activity in a
 CC mixed micelle assay with 1-palmitoyl-2-(14C) - arachidonyl-
 CC phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a
 CC lack of stimulation by ATP, and by including in its sequence at least one
 CC of the amino acid sequences given in AAW17839- 44). It is an
 CC alternatively spliced variant of another isolated polypeptide (AAW17845)
 CC and is encoded by an isolated cDNA (AAT68825). Other PLA2/B enzymes
 CC (AAW17846, AAW17848) have also been identified. sPLA2/B enzymes are
 CC thought to be involved in the release of arachidonic acid in specific
 CC tissues. Recombinant sPLA2/B polypeptides produced in transformed host
 CC cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory
 CC drugs which inhibit the arachidonic acid cascade
 XX Sequence 687 AA;
 SQ Query Match 100.0%; Score 2084; DB 2; Length 687;
 Best Local Similarity 100.0%; Pred. No. 6.8e-219;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQFFGRLVNTFGVTNLFNSNPRFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
 DB 1 MQFFGRLVNTFGVTNLFNSNPRFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
 QY 61 NPNRSQSGRLFQLELEADALVNFHQYSSQLLPFFYESSQVLTVEVLQHLTDLIRNHPWSW 120
 DB 61 NPNRSQSGRLFQLELEADALVNFHQYSSQLLPFFYESSQVLTVEVLQHLTDLIRNHPWSW 120
 QY 121 SVANHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDBILVELVQYCHTQMD 180
 DB 121 SVANHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDBILVELVQYCHTQMD 180
 QY 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNVNNGLTPLHLACQLGKQEMVRVLL 240
 DB 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNVNNGLTPLHLACQLGKQEMVRVLL 240
 QY 241 LCNARCNIIMPNGYPYTHSAMKFSQKCAEMISMDSSQHSQKDPYRGASPLHWAKNAEMA 300
 DB 241 LCNARCNIIMPNGYPYTHSAMKFSQKCAEMISMDSSQHSQKDPYRGASPLHWAKNAEMA 300
 QY 301 RMLLRKGCNNVNTSSAGNTALHGVNRRNPFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
 DB 301 RMLLRKGCNNVNTSSAGNTALHGVNRRNPFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
 QY 361 DNVEMIKALIVFGAEVDTNDFTGFTPTFLASKIG 394
 DB 361 DNVEMIKALIVFGAEVDTNDFTGFTPTFLASKIG 394
 RESULT 4
 ID ABB82231
 ID ABB82231 standard; protein; 687 AA.

XX ABB82231;
 XX AC
 XX DT
 XX DT
 XX DE Human cPLA2/B splice variant (clone 19a).
 XX
 XX Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
 KW antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;
 KW antiasthmatic; human.
 XX
 XX Homo sapiens.
 XX US2002106364-A1.
 XX PD 08-AUG-2002.
 XX PF 09-AUG-2001; 2001US-00927180.
 XX 27-JUL-1994; 94US-00281193.
 PR 14-APR-1995; 95US-00422106.
 PR 14-APR-1995; 95US-00422420.
 PR 26-JUN-1995; 95WO-US008069.
 PR 08-NOV-1995; 95US-00555568.
 PR 09-SEP-1998; 98US-00149988.
 PR 06-MAR-2000; 2000US-00519223.
 XX (GEMY) GENETICS INST INC.
 XX Jones S, Tang J;
 XX WPI; 2002-739923/80.
 DR N-PSDB; ABV73010.
 XX Novel composition comprising purified mammalian calcium independent
 PT phospholipase enzyme, useful for the screening of inhibitors of
 PT phospholipase activity, is active in the absence of calcium.
 XX Claim 6; Page 23-25; 41pp; English.
 XX The invention relates to a purified mammalian calcium independent
 CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
 CC characterized by activity in the absence of calcium and has a molecular
 CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
 CC calcium independent phospholipase enzyme is useful for identifying an
 CC inhibitor of phospholipase activity which involves combining (I),
 CC phospholipid and candidate inhibitor compound, and observing whether the
 CC enzyme cleaves the phospholipid and releases fatty acid from it. A
 CC pharmaceutical composition (PC) comprising a therapeutically effective
 CC amount of the inhibitor is useful for reducing inflammation and for
 CC treating inflammatory conditions including rheumatoid arthritis,
 CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
 CC by increased levels of prostaglandins, leukotriene or platelet activating
 CC factor. A composition comprising an antibody which binds to (I) is useful
 CC as research and diagnostic tool, and is also useful in the study of
 CC phospholipase A2 activity and inflammatory conditions. The present
 CC sequence represents a human cPLA2/B enzyme longer splice variant (clone
 CC 19a)
 XX Sequence 687 AA;
 SQ Query Match 100.0%; Score 2084; DB 5; Length 687;
 Best Local Similarity 100.0%; Pred. No. 6.8e-219;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQFFGRLVNTFGVTNLFNSNPRFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
 DB 1 MQFFGRLVNTFGVTNLFNSNPRFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
 QY 61 NPNRSQSGRLFQLELEADALVNFHQYSSQLLPFFYESSQVLTVEVLQHLTDLIRNHPWSW 120
 DB 61 NPNRSQSGRLFQLELEADALVNFHQYSSQLLPFFYESSQVLTVEVLQHLTDLIRNHPWSW 120

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XX      Sequence 394 AA;
SQ      Query Match
        Best Local Similarity 100.0%; Score 2084; DB 2; Length 394;
        Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MOFFGRLVNTFSGVNTLFSNPRVRKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB      1 MOFFGRLVNTFSGVNTLFSNPRVRKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60

QY      61 NPNRSQSGFRLFQLEADALVNFHQSQQLPFYESSPQVLHTEVLOHLDLIRNHPSW 120
DB      61 NPNRSQSGFRLFQLEADALVNFHQSQQLPFYESSPQVLHTEVLOHLDLIRNHPSW 120

QY      121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEIILVELVQYCHTQMD 180
DB      121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEIILVELVQYCHTQMD 180

QY      181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
DB      181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

QY      241 LCNARCNIIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB      241 LCNARCNIIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300

QY      301 RMLLKRGCVNSTSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHGTPLHLAMSK 360
DB      301 RMLLKRGCVNSTSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHGTPLHLAMSK 360

QY      361 DNVEMIKALIVFGAEVDTNDPGETPTFLASKIG 394
DB      361 DNVEMIKALIVFGAEVDTNDPGETPTFLASKIG 394

RESULT 2
ABB82229
ID      ABB82229 standard; protein; 394 AA.
AC      ABB82229;
XX
XX      08-JAN-2003 (first entry)
XX      Calcium independent phospholipase A2/B (cPLA2/B) (clone 19a).
XX      Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
KW      antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;
KW      antiasthmatic; human.
XX
OS      Homo sapiens.
XX
XX      US2002106364-A1.
XX
XX      08-AUG-2002.
XX
XX      09-AUG-2001; 2001US-00927180.
XX
XX      27-JUL-1994; 94US-00281193.
XX      14-APR-1995; 95US-00422106.
XX      14-APR-1995; 95US-00422420.
XX      26-JUN-1995; 95WO-05008069.
XX      08-NOV-1995; 95US-00555568.
XX      09-SEP-1998; 98US-00149988.
XX      06-MAR-2000; 2000US-00519223.
XX
XX      (GENY ) GENETICS INST INC.
XX
PI      Jones S, Tang J;
XX
XX      WPI: 2002-739923/80.
DR      N-PSDB; ABV73008.
XX

```

```

PT      Novel composition comprising purified mammalian calcium independent
PT      phospholipase enzyme, useful for the screening of inhibitors of
PT      phospholipase activity, is active in the absence of calcium.
PS      Claim 6; Page 18-19; 41pp; English.
XX
XX      The invention relates to a purified mammalian calcium independent
XX      cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
XX      characterized by activity in the absence of calcium and has a molecular
XX      weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
XX      calcium independent phospholipase enzyme is useful for identifying an
XX      inhibitor of phospholipase activity which involves combining (I),
XX      phospholipid and candidate inhibitor compound, and observing whether the
XX      enzyme cleaves the phospholipid and releases fatty acid from it. A
XX      pharmaceutical composition (PC) comprising a therapeutically effective
XX      amount of the inhibitor is useful for reducing inflammation and for
XX      treating inflammatory conditions including rheumatoid arthritis,
XX      psoriasis, asthma, inflammatory bowel disease and other diseases mediated
XX      by increased levels of prostaglandins, leukotriene or platelet activating
XX      factor. A composition comprising an antibody which binds to (I) is useful
XX      as research and diagnostic tool, and is also useful in the study of
XX      phospholipase A2 activity and inflammatory conditions. The present
XX      sequence represents a human cPLA2/B enzyme (clone 19a)
XX
SQ      Sequence 394 AA;

Query Match      100.0%; Score 2084; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 2,7e-219;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MOFFGRLVNTFSGVNTLFSNPRVRKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB      1 MOFFGRLVNTFSGVNTLFSNPRVRKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60

QY      61 NPNRSQSGFRLFQLEADALVNFHQSQQLPFYESSPQVLHTEVLOHLDLIRNHPSW 120
DB      61 NPNRSQSGFRLFQLEADALVNFHQSQQLPFYESSPQVLHTEVLOHLDLIRNHPSW 120

QY      121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEIILVELVQYCHTQMD 180
DB      121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEIILVELVQYCHTQMD 180

QY      181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
DB      181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

QY      241 LCNARCNIIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB      241 LCNARCNIIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300

QY      301 RMLLKRGCVNSTSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHGTPLHLAMSK 360
DB      301 RMLLKRGCVNSTSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHGTPLHLAMSK 360

QY      361 DNVEMIKALIVFGAEVDTNDPGETPTFLASKIG 394
DB      361 DNVEMIKALIVFGAEVDTNDPGETPTFLASKIG 394

RESULT 3
AAW17847
ID      AAW17847 standard; protein; 687 AA.
XX
XX      AAW17847;
XX
XX      07-AUG-1997 (first entry)
XX
XX      Cytosolic phospholipase A2/B (alternatively spliced clone 19a).
DE
XX
XX      Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
KW      inflammation; inhibitor; antiinflammatory.
XX
XX      Homo sapiens.
OS

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:05:39 ; Search time 50.851 Seconds

(without alignments)
2996.666 Million cell updates/sec

Title: US-10-612-668-17

Perfect score: 2084

Sequence: 1 MQFRLVNTFSGVNLFNS.....EVDTFNDFGETPTFLASKIG 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2084	100.0	394	2	AAW17845	Aaw17845 Cytosolic
2	2084	100.0	394	5	ABB82229	Abb82229 Calcium i
3	2084	100.0	687	2	AAW17847	Aaw17847 Cytosolic
4	2084	100.0	687	5	ABB82231	Abb82231 Human cpl
5	2084	100.0	688	2	AAW17848	Aaw17848 Cytosolic
6	2084	100.0	688	5	ABB82232	Abb82232 Human cpl
7	2078	99.7	784	7	ADD93407	Add93407 Human lip
8	2078	99.7	806	5	AAE25968	Aae25968 Human pla
9	2078	99.7	806	8	AD019776	Ado19776 Human pro
10	2054	98.6	810	8	ABM84355	Abm84355 Human dia
11	2054	98.6	810	8	ABM84354	Abm84354 Human dia
12	1837	88.1	752	2	AAR83018	Aar83018 Calcium-i
13	1837	88.1	752	2	AAW01479	Aaw01479 Calcium-i
14	1837	88.1	752	2	AAW13163	Aaw13163 Ca-indepe
15	1837	88.1	752	2	AAW17849	Aaw17849 Hamster c
16	1837	88.1	752	2	AAW81825	Aaw81825 Chinese h
17	1837	88.1	752	5	ABB82215	Abb82215 Calcium i
18	1808.5	86.8	751	7	ADDA46244	Add46244 Rat Prote
19	1808.5	86.8	751	7	ADE60532	Ades60532 Rat Prote
20	1808.5	86.8	751	7	ADE55230	Ades55230 Rat Prote
21	1808.5	86.8	751	7	ADE60536	Ades60536 Rat Prote
22	1234.5	59.2	667	7	ADM05093	Adm05093 Human pro
23	836	40.1	401	4	AAB92811	Aab92811 Human pro
24	494.5	23.7	877	4	ABB62624	Abb62624 Drosophil
25	338	16.2	843	7	ADD27861	Add27861 Rat ankyr

ALIGNMENTS

RESULT 1

AAW17845

ID AAW17845 standard; protein; 394 AA.

XX

AC AAW17845;

XX

DT 07-AUG-1997 (first entry)

XX

DE Cytosolic phospholipase A2/B (clone 19a product).

XX

KW Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;

KW inflammation; inhibitor; antiinflammatory.

OS Homo sapiens.

XX

FN WO9717448-A2.

XX

PD 15-MAY-1997.

XX

PF 07-NOV-1996; 96WO-US017794.

XX

PR 08-NOV-1995; 95US-00555568.

XX

(GEMY) GENETICS INST INC.

PA Jones S, Tang J;

XX

WPI; 1997-281037/25.

DR N-PSDB; AAT68823.

XX

Calcium independent phospholipase A2/B - used to reduce inflammation in a mammalian subject.

PT Claim 12; Page 43-44; 74pp; English.

XX

PS A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17845) is characterised by activity in the absence of calcium, by activity in a mixed micelle assay with 1-palmitoyl-2-(14C)- arachidonyl-phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a lack of stimulation by ATP, and by including in its sequence at least one of the amino acid sequences given in AAW17839- 44). It is encoded by partial cDNA clone 19a (AAT68823), derived from Burkitt's lymphoma Raji (ATCC CRL86) cells. Other PLA2/B enzymes (AAW17846-48) have also been identified. sPLA2/B enzymes are thought to be involved in the release of arachidonic acid in specific tissues. Recombinant sPLA2/B polypeptides produced in transformed host cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory drugs which inhibit the arachidonic acid cascade

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FT	REPEAT	1939	1950	Repeat A.
FT	DOMAIN	3536	3620	Death.
FT	VARSP LIC	1039	1039	Q -> QFLGKHLHPTAPPPLNEGESLVSRILQLGPPGTK
FT				(in isoform 2).
FT	VARSP LIC	1444	3528	/FTId=VSP_000267.
FT				Missing (in isoform 2 and isoform 3).
FT	CONFLICT	475	476	/FTId=VSP_000268.
FT	CONFLICT	971	971	GQ -> PE (in Ref. 4).
FT	CONFLICT	3581	3582	I -> S (in Ref. 1).
FT	CONFLICT	3586	3586	OY -> HA (in Ref. 1).
FT	CONFLICT	3586	3586	I -> Y (in Ref. 1).
SQ	SEQUENCE	3924	AA; 430337	MW; 52AC496C428E29D2 CRC64;
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QY	103	HTEVLQHLTD-----LIRNHPWSVAHLAVELGIRECFHH-----SRII	141	
Db	311	HQVVELLERGAPLLARTKNGLSPLHMAAQGDHVECVKHLLOHKAPVDDVTLDYLTALH	370	
QY	142	SCANC-----AENEECTPLHLACRKGDEILVELVQY-----	174	
Db	371	VAHCGHYRVTKLLDKRANPNARALNGFTPLHIACKKRIKVMELLVKYGASIQAITES	430	
QY	175	-----CH-----TQMDVTYKGETVEHYVQGDNSQVLOLLGRNAVAG	212	
Db	431	GLTPIHVAAPMGHINIVLLLLQNGASPDVTINIRGETALHWAARAGQVEVVRCLLRNG-AL	489	
QY	213	LNQVNNQGLTPLHLACQLKQEMVRVLLLCNARCINIMPGNY-PIHSAMKFSQKCAEMI	271	
Db	490	VDARAREEQTLHIASRLGKTEIVQLLQHMAHPDAATTNGYTPLHISAREGQVDVASVL	549	
QY	272	ISWDSQIHKDPRYCASPLHWAK---NAEMAMLLKRCGNVNSTSSAGNTALHVGWMRN	328	
Db	550	--LEAGAAHSLATKKGFTPLHVAAKYGSGLDVAKLLQRRRAADSAGKNGLTPLHVAHYD	607	
QY	329	RFDCAIVLLTHGANADARGEHNGTPLHLAMSNDNEMIKALIVFGAEVDTPNDFGETPTF	388	
Db	608	NOKVALLLEKASPHATKNGYTPUHIAAKNQMOIASTLLNYGAETNIVTKQGVTPUH	667	
QY	389	LASKIG	394	
Db	668	LASQEG	673	

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Job time : 69.0417 secs

RA the FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Retina;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Retina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
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 RC STRAIN=C57BL/6J; TISSUE=Retina;
 RX Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Tanahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK044634; BAC32012.1; --
 DR HSSP; P16157; 1N11
 DR MGD; MG1:89025; Ank2.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00023; Ank; 23.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01415; ANKYRN.
 DR SMART; SM00248; ANK; 23.
 DR PROSITE; PS0088; ANK_REPEAT; 20.
 DR PROSITE; PS0297; ANK_REPEAT; 1.
 DR ANK repeat.
 KW ANK repeat.
 FT NON TER
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 DB 307 HQQVVELLERKAPLLARTKNGLSPLHMAAQGDHVECVKHLQYKAPVDVTLDTLH 366
 QY 142 SCANC-----AENEEGCTPLHACRKGDELIVELY-----174
 DB 367 VAAHCGHYRVTKLLDKRANPNARALNGFTPLHIAKKNRIKVMELLYKYGASIQAITES 426
 QY 175 -----CH-----TQMDVTDYKGETVFHYVAGQDINSQVLLGRNAVAG 212
 DB 427 GLTPIHVAAFMGHNLIVLLLLQNGASPDVTNIRGETALHMAARAGQVGVVRCILRNG-AL 485

QY 213 LQVNNQGLTPLHLACQLGKQEMVRVLLLCNARCINMGPNGY-PIHSAMKFSQKGAEMI 271
 DB 486 VVARAREEQTPHIAIRLKGTEIVQLLQHMHPDAATNGYTPHLHISAREGQVDVASVL 545
 QY 272 ISMDSQIHSKDPYRGASPLHWAK---NAEMARMLLKRCNCNVNSTSSAGNTALHVGVMRN 328
 DB 546 --LEAGAAHSLATKKGFTPLHVAAYKGLDVAKLLQRRAAADSAGKNGLTPHLHVAHYD 603
 QY 329 RFDCAIVLTHGANADARGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTPNDFGETPTF 388
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 QY 389 LASKIG 394
 DB 664 LASQEG 669
 RESULT 14
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 AC Q7Z3L5;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein DKPZp686H0688.
 GN Name=DKPZp686H0688;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human retina;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX537758; CAD97827.1; --
 DR HSSP; P55271; 1D9S.
 DR GO; GO:0005515; F:protein binding; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00023; Ank; 23.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00791; ZU5; 1.
 DR SMART; SM00248; ANK; 23.
 DR SMART; SM00005; DEATH; 1.
 DR PROSITE; PS0088; ANK_REPEAT; 20.
 DR PROSITE; PS0297; ANK_REPEAT; 1.
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 QY 142 SCANC-----AENEEGCTPLHACRKGDELIVELY-----174
 DB 350 VAAHCGHYRVTKLLDKRANPNARALNGFTPLHIAKKNRIKVMELLYKYGASIQAITES 409
 QY 175 -----CH-----TQMDVTDYKGETVFHYVAGQDINSQVLLGRNAVAG 212
 DB 410 GLTPIHVAAFMGHNLIVLLLLQNGASPDVTNIRGETALHMAARAGQVGVVRCILRNG-AL 468
 QY 213 LQVNNQGLTPLHLACQLGKQEMVRVLLLCNARCINMGPNGY-PIHSAMKFSQKGAEMI 271


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CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008968; EAA13225.1; -.
DR HSSP; P20749; 1K1B.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000560; HisAc_phosphatase.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR PRINTS; PR01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PROSITE; PS50088; ANK REPEAT; 3.
DR PROSITE; PS50297; ANK REP REGION; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW ANK repeat.
FT NON TER 1
FT NON TER 879
FT NON TER 879
SQ SEQUENCE 879 AA; 96484 MW; 3491E003CF637188 CRC64;

Query Match 24.6%; Score 512; DB 2; Length 879;
Best Local Similarity 29.8%; Pred. No. 3.1e-33;
Matches 113; Conservative 81; Mismatches 175; Indels 10; Gaps 5;

QY 21 PPRVKEVAVADYTSDDRVREBQQLILFQNTPNR-----TWDCVLVNPNS--QSGFRLPQ 73
DB 11 PKVQEVKNESINLPVLQRNESMRLFAPNPNSPDKLVYEILRPHSETINTSYSLYR 70
QY 74 LELEADALVNFQYSSQLLPFFESSPOVLHTEVLHLDLIRNHPNSWSVAHLAVELGTR 133
DB 71 ATTQSAEKEFPAHORELPVLPVLYREMNYINGLQKCDVLIDNPSWSLAHVAFNLTD 130
QY 134 CFHHSRIISCAENAEBCETPLHLACRGDGEILVELVQYCHTQMDVTDYKGTVFHYA 193
DB 131 YISNPSIIDFLDYAEYSMTPLQVAVKANNIEFVKALIQSQCNLEHLDKNSVFHYA 190
QY 194 VQDINSQVQLLGRNAVAGLNQVNOGLTPLHLACOLGQEMVRVLLLCNARCINMGPN 253
DB 191 A-STTKEMINMLTATSTSNLNHCNTDGYTPLHLACLADPCVKALLAGADTNKMA-RG 248
QY 254 YPIHSAMKFSQKGCAMISDSSQHSKDPYASPLHWAKNAEMWMLLRKGCNVNST 313
DB 249 AGTSYSKSTPSSNVADFLVS-NPNKLFQDMKGGTPLHWSSRVLSLIERGGDVLNV 307
QY 314 SSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSKNVEMKALIVRG 373
DB 308 NFNGQTPLHVMVARDLECVALLAHDAIDVDVDSNGNTPLHIAVEKKLPIVQCLVWFG 367
QY 374 AEVDTPNDPGETPTFLASK 392
DB 368 ADFNFKPKDGKTPRHLVGK 386

RESULT 10
QYV760 PRELIMINARY; PRT; 877 AA.
ID AC Q9VT60;
AC Q9VT60;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG6718-PA.
GN ORFNames=CG6718;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazew R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Bencos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Fiegler A., Frazar C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN [5]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
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RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Pancreatic islets;
 RX MEDLINE=97269008; PubMed=9111008; DOI=10.1074/jbc.272.17.11250;
 RA Ma Z., Ramanadham S., Kempe K., Chi X.S., Ladenson J., Turk J.;
 RT "Pancreatic islets express a Ca²⁺-independent phospholipase A2 enzyme
 RT that contains a repeated structural homologous to the integral
 RT membrane protein binding domain of ankyrin.";
 RL J. Biol. Chem. 272:11118-11127(1997).
 CC -!- FUNCTION: Catalyzes the release of fatty acids from phospholipids.
 CC It has been implicated in normal phospholipid remodeling, nitric
 CC oxide-induced or vasopressin-induced arachidonic acid release and
 CC in leukotriene and prostaglandin production. May participate in
 CC fas mediated apoptosis and in regulating transmembrane ion flux in
 CC glucose-stimulated B-cells.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a carboxylate.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Found in brain, lung, spleen, kidney, liver,
 CC heart and skeletal muscle.
 CC -!- SIMILARITY: Contains 7 ANK repeats.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U51898; AAC53136.1; -;
 DR HSP; Q60778; I0Y3.
 DR GSD; 628867; Fla2g6.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; Ank; 6.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 6.
 DR PROSITE; PS50088; ANK_REPEAT; 4.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KW ANK repeat; Hydrolase; Lipid degradation; Repeat.
 FT REPEAT 150 180 ANK 1.
 FT REPEAT 184 214 ANK 2.
 FT REPEAT 218 247 ANK 3.
 FT REPEAT 250 280 ANK 4.
 FT REPEAT 285 311 ANK 5.
 FT REPEAT 315 344 ANK 6.
 FT REPEAT 348 377 ANK 7.
 FT ACT SITE 464 464 Potential.
 SQ SEQUENCE 751 AA; 83582 MW; 393BBBADA7FCC99B CRC64;
 Query Match 86.8%; Score 1808.5; DB 1; Length 751;
 Best Local Similarity 86.8%; Pred. No. 4.6e-140;
 Matches 341; Conservative 20; Mismatches 31; Indels 1; Gaps 1;
 QY 1 MOFFGLVNTFGVNTLFSNPRVKEVAVADYTSSDRVEEGQLILFQNTNRTWDCVLV 60
 DB 1 MOFFGLVNTLSSVNTLFSNPRVKEVAVADYTSSDRVEEGQLILFQNTNRTWDCVLV 60
 QY 61 NFRNSQSGFRLFOLEADALNFHVOYSSQLLPFYESSPQVLHTEVLQHLTLIRNHPWS 120
 DB 61 SPNPNQSDRLFOLESEADVLNVNQYSSQLPFYESSQVLHVEVLQ-LTDLIRNHPWS 119
 QY 121 SVAHLAVELGIRECFHHSRIISCANCAENBEGCTPLHLACRKGDSILVELVOYCHTQMD 180
 DB 120 TVTHLAVELGIRECFHHSRIITCANSTENEGCTPLHLACRKGDSILVELVOYCHTQMD 179
 QY 181 VTDYKGETVTHAVQGDNSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGQEMVRVLL 240
 DB 180 VTDNKGETAFAHVAQGDNPQVLQLLGNKASAGLNVNNOGLTPLHLACQMGQEMVRVLL 239
 QY 241 LCNARCNMGPNGYPTHSAKTSQKCAEMITSMDSQIHSKDPRYGASPLHWAKNAENA 300
 DB 240 LCNARCNMGPGFPHTAKTSQKCAEMITSMDSNQIHSKDPRYGASPLHWAKNAENA 299

QY 301 RMLLRGCGNVNSTSAGNTALHVGVMRFDCAIVLLTHGANADARGHGNTPLHLAMSK 360
 DB 300 RMLLRGCGVDSTSGNTALHVAVTRNFDCAIVLLTHGANAGARGHGNTPLHLAMSK 359
 QY 361 DNVEIKALIVFGAEVDTPNDFGETPTFLASKI 393
 DB 360 DNMEVAKALIVFGAEVDTPNDFGETPTAFIASKI 392
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 AC Q6DDKO;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE MGC83523 protein.
 GN Name=MGC83523;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shremen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalilus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC077558; AAH77558.1; -;
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002641; Patatin.
 DR Pfam; PF00023; Ank; 7.
 DR Pfam; PF01734; Patatin; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 7.
 DR PROSITE; PS50088; ANK_REPEAT; 3.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KW ANK repeat.

RA Balboa M.A., Balseinde J., Jones S.S., Dennis E.A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalious D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
acylglycerophosphocholine + a carboxylate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Contains 7 ANK repeats.
CC -----
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CC -----
DR EMBL; U88624; AAB48511.2; -;
DR EMBL; BC003487; AAB03487.1; -;
DR HSP; Q60778; 10Y3.
DR MGD; MGI:1859152; Pla296.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ANK; 6.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT; 1.
KW ANK repeat; Hydrolase; Lipid degradation; Repeat.
FT REPEAT 151 181 ANK 1.
FT REPEAT 185 215 ANK 2.
FT REPEAT 219 248 ANK 3.
FT REPEAT 251 281 ANK 4.
FT REPEAT 286 312 ANK 5.
FT REPEAT 316 345 ANK 6.
FT REPEAT 349 378 ANK 7.
FT ACT SITE 465 465 Potential.
SQ SEQUENCE 752 AA; 83702 NW; AAC3347B0E1292E9 CRC64;

Query Match 88.4%; Score 1842; DB 1; Length 752;
Best Local Similarity 87.8%; Pred. No. 8e-143;
Matches 345; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 1 MQFFGLVNTFSGVNLNFSNPRVKEVAVADYTSRRVREEQQLILFQNTNRTWDCVIL 60
DB 1 MQFFGLVNTLSSVTLNFSNPRVKEVSLTDYVSSRVEREQQLILLQNVSNRTWDCVIL 60

QY 61 NPNRSQSGRLPQLEADALNPHQYSSQLLPFYESSQVILHTVQLHTLDIRNPSW 120
DB 61 SPRNFQSGRLPQLESEADALNPHQYSSQLPFYESSQVILHTVQLHTLDIRNPSW 120

QY 121 SVAHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRGDSEILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRGDSEILVELVOYCHTQMD 180

Db 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRGDSEILVELVOYCHTQMD 180
QY 181 VTDYKGETVPHYVQGDNSQVQLLGRNAVAGLQVNNQGLTPLHLACOLGQKQEMVRVLL 240
Db 181 VTDNKGETAHYVQGDNPQVQLLQKNASAGLQVNNQGLTPLHLACMGKQEMVRVLL 240
QY 241 LCNARCNITMGNGVPIHSAKFQSGKCAEMILISMDSSQIHSDKDPYRGASPLHWAKNAWA 300
Db 241 LCNARCNITMGNGVPIHSAKFQSGKCAEMILISMDSSQIHSDKDPYRGASPLHWAKNAWA 300
QY 301 RMLLKRCGNVNSTSSAGNTALHVGVMRNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLKRCGVDVSTSSGNTALHVAVMRNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNEMIKALIVFGAEVDPNDPFGETPTPLASKI 393
Db 361 DNEMVVKALIVFGAEVDPNDPFGETPTPLASKI 393

RESULT 4
Q9JK61 PRELIMINARY; PRT; 807 AA.
AC Q9JK61;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ca2+-independent phospholipase A2 long form (Pla296 protein).
GN Name=Pla296;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIH/Swiss;
RA Chiu C.-H., Jackowski S.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalious D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF259401; AAF72651.1; -;
DR EMBL; BC057209; AAH57209.1; -;
DR HSP; Q60778; 10Y3.
DR MGD; MGI:1859152; Pla296.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.

DR HSP; Q60778; 10Y3.
DR Genew; HGNC:9039; PLA2G6.

Query Match 99.7%; Score 2078; DB 1; Length 806;
Best Local Similarity 99.7%; Pred. No. 3.3e-162;
Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTLNFSNPRFRVKEVAVADYTSSDRVEEGQLILFQNTPNRTWDCVLY 60
Db 1 MOFFGRLVNTFSGVTLNFSNPRFRVKEVAVADYTSSDRVEEGQLILFQNTPNRTWDCVLY 60

QY 61 NPNRSGGRLPQLLEADALVNFHQSOLLPPFYESSQVLHTEVQLHQLTDLIRNHPW 120
Db 61 NPNRSGGRLPQLLEADALVNFHQSOLLPPFYESSQVLHTEVQLHQLTDLIRNHPW 120

QY 121 SVHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDSILVELVOYCHTQMD 180
Db 121 SVHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDSILVELVOYCHTQMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVLQGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDYKGETVFHYAVQGDNSQVLQGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

QY 241 LCNARCINMGPNYPHSAKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCINMGPNYPHSAKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300

QY 301 RMLKRGCCNVNSTSSAGNTALHGVNVRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLKRGCCNVNSTSSAGNTALHGVNVRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360

QY 361 DNVEIMKALIVFGAEVDTNDPFGETPTFLASKIG 394
Db 361 DNVEIMKALIVFGAEVDTNDPFGETPTFLASKIG 394

RESULT 2
ID Q66HD1 PRELIMINARY; PRT; 807 AA.
AC Q66HD1;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeb B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina X., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC081916; AAH81916.1; -.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR PRINTS; PR01734; Patatin; 1.
DR SMART; SM00248; Ank; 6.
DR PROSITE; PS50088; ANK REPEAT; 4.
DR PROSITE; PS50297; ANK REP REGION; 1.
KW ANK repeat, Hypothetical protein.
SQ SEQUENCE 807 AA; 89555 MW; 1B9018AE1B2D252F CRC64;

Query Match 88.8%; Score 1851; DB 2; Length 807;
Best Local Similarity 88.3%; Pred. No. 1.6e-143;
Matches 347; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTLNFSNPRFRVKEVAVADYTSSDRVEEGQLILFQNTPNRTWDCVLY 60
Db 1 MOFFGRLVNTLSSVTLNFSNPRFRVKEVSLADYASSRVEREGLIILLQNASNRTWDCVLY 60

QY 61 NPNRSGGRLPQLLEADALVNFHQSOLLPPFYESSQVLHTEVQLHQLTDLIRNHPW 120
Db 61 SPRNPQSGRLPQLLEADALVNFQYSSQLPPFYESSQVLHTEVQLHQLTDLIRNHPW 120

QY 121 SVHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDSILVELVOYCHTQMD 180
Db 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRKGDSILVELVOYCHQAMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVLQGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDNGETAFHYAVQGDNPQVLQGRNASAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

QY 241 LCNARCINMGPNYPHSAKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCINMGPGFPHTAMKFSQKCAEMIIISMDNQIHSKDPYRGASPLHWAKNAEMA 300

QY 301 RMLKRGCCNVNSTSSAGNTALHGVNVRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLKRGCCDVSASGNTALHVAVTNRNFDCAIVLLTYCANAGARGEHNTPLHLAMSK 360

QY 361 DNVEIMKALIVFGAEVDTNDPFGETPTFLASKI 393
Db 361 DNNEWMKALIVFGAEVDTNDPFGETPAFIASKI 393

RESULT 3
PA26 MOUSE
ID PA26 MOUSE STANDARD; PRT; 752 AA.
AC P97819; Q99LA9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (CaI-PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=Pla2g6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RX MEDLINE=97236816; PubMed=9079688; DOI=10.1074/jbc.272.13.8576;
RA Balboa M.A., Balsinde J., Jones S.S., Dennis E.A.;
RT "Identity between the Ca2+-independent phospholipase A2 enzymes from
P38D1 macrophages and Chinese hamster ovary cells.";
RL J. Biol. Chem. 272:8576-8580(1997).
RN [2]
RP REVISIONS TO 2-3; 9; 11 AND 211.

[6]
 RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
 RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
 RA Clump M., Smith L.J., Anscough R., Almeida J.P., Babbage A.K.,
 RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
 RA Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,
 RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
 RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
 RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
 RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
 RA Hunt S.B., Jones M.C., Kershaw J., Kimberley A.M., King A.,
 RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd O.T.,
 RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann M.,
 RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
 RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
 RA Vaadin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Minoshima S., Shibuya K., Sasaki T., Asakawa S., Kudon J.,
 RA Shintani A., Kibayashi K., Yoshizaki Y., Aoki N., Mitsuoyama S.,
 RA Roe B.A., Chen F., Chu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
 RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
 RA Fullon R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
 RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
 RA Korfi I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
 RA Wilson R., Emanuel B.S., Shaikh T., Kuraishi H., Saitta S.,
 RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
 RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
 RA Peyrard M., Kedra D., Seroussi E., Franssion I., Tapia I., Bruder C.E.,
 RA O'Brien K.P., Wilkinson P., Bodenreich A., Hartman K., Hu X.,
 RA Khan A.S., Lane L., Tilahun Y., Wright H.;
 RA "The DNA sequence of human chromosome 22.";
 RL Nature 402:489-495(1999).
 [7]
 RP SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2).
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stacievski M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustun T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Catalyzes the release of fatty acids from phospholipids.
 CC It has been implicated in normal phospholipid remodeling, nitric
 CC oxide-induced or vasopressin-induced arachidonic acid release and

in leukotriene and prostaglandin production. May participate in
 fas mediated apoptosis and in regulating transmembrane ion flux in
 glucose-stimulated B-cells.
 -!- FUNCTION: Isoform ankryrin-iPLA2-1 and isoform ankryrin-iPLA2-2,
 which lack the catalytic domain, are probably involved in the
 negative regulation of iPLA2 activity.
 -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 acylglycerophosphocholine + a carboxylate.
 -!- SUBUNIT: Forms large oligomeric 270-350 kDa structures.
 -!- SUBCELLULAR LOCATION: Isoform LH-IPLA2 was found to be membrane
 bound. Isoform SH-IPLA2 is cytoplasmic.
 -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=4;
 CC Name=LH-IPLA2;
 CC IsoId=O60733-1; Sequence=Displayed;
 CC Name=SH-IPLA2;
 CC IsoId=O60733-2; Sequence=VSP_000278;
 CC Name=Ankryrin-iPLA2-1;
 CC IsoId=O60733-3; Sequence=VSP_000281, VSP_000282;
 CC Name=Ankryrin-iPLA2-2;
 CC IsoId=O60733-4; Sequence=VSP_000277, VSP_000279, VSP_000280;
 CC -!- TISSUE SPECIFICITY: Four different transcripts were found to be
 expressed in a distinct tissue distribution.
 CC -!- SIMILARITY: Contains 7 ANK repeats.

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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 CC EMBL; AF064594; AAC97486.1; -
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 CC EMBL; AF102989; AAD41723.1; -
 CC EMBL; AF117692; AAD30424.1; JOINED.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:06:44 ; Search time 64.0417 Seconds
(without alignments)

3150.433 Million cell updates/sec

Title: US-10-612-668-17

Perfect score: 2084

Sequence: 1 MQFFRLVNTFSGVNLFNSN.....EVDTPNDFGTPTFLASKIG 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2078	99.7	806	1	PA26 HUMAN	O60733 homo sapien
2	1851	88.8	807	1	Q66HD1	Q66hd1 rattus norv
3	1842	88.4	752	1	PA26 MOUSE	P97819 mus musculu
4	1842	88.4	807	2	Q9JK61	Q9jk61 mus musculu
5	1832	87.9	752	2	Q7TPX2	Q7tpx2 rattus norv
6	1808.5	86.8	751	1	PA26 RAT	P97570 rattus norv
7	1176	56.4	756	2	Q6DDK0	Q6ddk0 xenopus lae
8	1037.5	49.8	818	2	Q6NXY0	Q6nxy0 brachydanio
9	512	24.6	879	2	Q7Q2U1	Q7q2u1 anopheles g
10	494.5	23.7	877	2	Q9VT60	Q9vt60 drosophila
11	494.5	23.7	887	2	Q7KUD4	Q7kud4 drosophila
12	338	16.2	843	2	P97582	P97582 rattus norv
13	338	16.2	1219	2	Q8C8R3	Q8c8r3 mus musculu
14	332	15.9	1863	2	Q723L5	Q723l5 homo sapien
15	332	15.9	3924	1	ANK2 HUMAN	Q01484 homo sapien
16	318	15.3	1004	2	Q7JNZ0	Q7jnz0 caenorhabdi
17	318	15.3	1786	2	Q17344	Q17344 caenorhabdi
18	318	15.3	1809	2	Q17487	Q17487 caenorhabdi
19	318	15.3	1815	2	Q17488	Q17488 caenorhabdi
20	318	15.3	1841	2	Q8MQG0	Q8mqg0 caenorhabdi
21	318	15.3	1867	2	Q17486	Q17486 caenorhabdi
22	318	15.3	2039	2	Q17489	Q17489 caenorhabdi
23	318	15.3	6994	2	Q17343	Q17343 caenorhabdi
24	318	15.3	6994	2	Q17490	Q17490 caenorhabdi
25	313.5	15.0	1549	2	Q24241	Q24241 drosophila
26	313.5	15.0	1549	2	Q9V4B1	Q9v4b1 drosophila
27	310	14.9	1009	2	Q8SWY2	Q8swy2 drosophila
28	310	14.9	1159	2	Q9NCP8	Q9ncp8 drosophila
29	310	14.9	1571	2	Q7KUR2	Q7kur2 drosophila
30	305.5	14.7	792	2	Q7Q172	Q7q172 anopheles g
31	304.5	14.6	820	2	Q8JHU3	Q8jhu3 brachydanio

32	301	14.4	786	2	Q9ERK0	Q9erk0 mus musculu
33	298	14.3	2622	2	Q70511	Q70511 rattus norv
34	296	14.2	1088	2	Q13484	Q13484 homo sapien
35	296	14.2	4377	1	ANK3 HUMAN	Q12955 homo sapien
36	295.5	14.2	1145	2	Q7FEZ8	Q7pez8 anopheles g
37	295.5	14.2	1501	2	Q7QKD3	Q7qkd3 anopheles g
38	295	14.2	1887	2	Q7Z3G4	Q7z3g4 homo sapien
39	294.5	14.1	1136	2	Q9N180	Q9n180 bos taurus
40	294	14.1	1719	2	Q13768	Q13768 homo sapien
41	294	14.1	1856	2	Q99407	Q99407 homo sapien
42	294	14.1	1880	1	ANK1 HUMAN	P16157 homo sapien
43	293	14.1	1726	2	Q8VC68	Q8vc68 mus musculu
44	293	14.1	1943	2	Q61307	Q61307 mus musculu
45	290.5	13.9	1614	2	Q7TIG6	Q7tig6 brachydanio

ALIGNMENTS

RESULT 1

PA26_HUMAN STANDARD; PRT; 806 AA.
AC O60733; Q75645; Q8N452; Q9UG29; Q9UIT0; Q9Y671;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (CaI-PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=PLA2G6; Synonyms=IPLA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2; ANKYRIN-IPLA2-1 AND ANKYRIN-IPLA2-2).
RC TISSUE=B-cell, and Testis;
RX MEDLINE=98079046; PubMed=9417066; DOI=10.1074/jbc.273.1.207;
RA Larsson P.K.A., Claesson H.-E., Kennedy B.P.;
RT "Multiple splice variants of the human calcium-independent phospholipase A2 and their effect on enzyme activity.";
RL J. Biol. Chem. 273:207-214 (1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2).
RC TISSUE=pancreatic islets;
RX MEDLINE=99194813; PubMed=10092647; DOI=10.1074/jbc.274.14.9607;
RA Ma Z., Wang X., Nowatzke W., Ramanadham S., Turk J.;
RT "Human pancreatic islets express mRNA species encoding two distinct catalytically active isoforms of group VI phospholipase A2 (iPLA2) that arise from an exon-skipping mechanism of alternative splicing of the transcript from the iPLA2 gene on chromosome 22q13.1.";
RL J. Biol. Chem. 274:9607-9616 (1999).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=99269033; PubMed=10336645;
RA Larsson Forsell P.K.A., Kennedy B.P., Claesson H.-E.;
RT "The human calcium-independent phospholipase A2 gene. Multiple enzymes with distinct properties from a single gene.";
RL Eur. J. Biochem. 262:575-585 (1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM LH-IPLA).
RC TISSUE=Testis;
RX Ansong W., Winkner U., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS ILE-58; GLY-63; GLN-70; ASN-183 AND THR-343.
RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Sherwood A.M., Leithauer B.J., Nickerson D.A.;
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1862 <RS>

A:Cross-references: UNIPROT:Q02357; GB:M84756; NID:g191939; PIDN:AAA37236.1; PID:g191940

C:Genetics:

A:Gene: Ank-1

C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing

F:40-72/Domain: ankyrin repeat homology <AN01>

F:73-105/Domain: ankyrin repeat homology <AN02>

F:106-138/Domain: ankyrin repeat homology <AN03>

F:139-167/Domain: ankyrin repeat homology <AN04>

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F:762-794/Domain: ankyrin repeat homology <AN23>

Query Match 13.7%; Score 285; DB 2; Length 1862;

Best Local Similarity 25.6%; Pred. No. 1.7e-15;

Matches 93; Conservative 55; Mismatches 121; Indels 94; Gaps 10;

QY 107 LOHLDLIRNHPFSWSVAHLAVELGIRECPHH--SRIISCANCAENE---EGCTPLHLACR 161

DB 332 LDHLTPL-----HVAA-----HCGHHRVAKVLLDKGAKPNRSLNGFTPLHIACK 376

QY 162 KGDGEILVELVQYCHTQMD-----VTDYKGET 188

DB 377 KKHIRMV-ELLKKTGASIDAVTESGLTPLHVASFMGHLPIVKVNLQORGASPNVSNKVT 435

QY 189 VHYAVQGDNSQVLOLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLLCNARCN 248

DB 436 PLHMAARAGHTEVAKYLLQNK-AKANAKAQDQTPHCAARIGTGMVKLLLENGASPNL 494

QY 249 MGPNGY-----PIHSAMKFSQKGCACMIISM 274

DB 495 ATTAGHTPLHTAAREGHVDTALALLEKEASQACMTKKGFTPLHVAAKYGVKVLAEILLLEH 554

QY 275 DSSQIHSKDPYRGASPLHWA---KNAEMARMLKRCNVNSTSSAGNTALHVGVMNRNFD 331

DB 555 DAHP--NAAGKNGLTPLHVAHVHNNLDIVKLLPRGGSHPSPAWNGYTPHLHAAKQNGIE 612

QY 332 CAIVLTHGANADARGEHNTPLHLMSKDNVEMIKALIVFGAEVDTNDFGCTPTFLAS 391

DB 613 VARSLLQYGSANAESVQGVTPHLHAAQEGHTEWALLLSKQANGNLGNKSGLTPLHLVS 672

QY 392 KIG 394

DB 673 QEG 675

RESULT 15

T46445

hypothetical protein DKFp434B2328.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C:Accession: T46445

R:Blocker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, January 2000

A:Reference number: Z23032

A:Accession: T46445

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-397 <AAA>

A:Cross-references: UNIPROT:O9NTAL; EMBL:AL137448

A:Experimental source: adult testis; clone DKFZp434B2328

C:Genetics:

A:Note: DKFZp434B2328.1

Query Match

Best Local Similarity 13.5%; Score 281.5; DB 2; Length 397;

Matches 86; Conservative 48; Mismatches 135; Indels 11; Gaps 7;

QY 121 SVAHLAVELGIRECPHHHSRIISCANCAENEECTPLHLAC-RKGDGEILVELVQYCHTOM 179

DB 53 SLLHLAVEAGQECACAKWLLNANPNLSNRRGSTPLHMAVERVRG--VVELLARKISV 110

QY 180 DVTDYKGETVHYAVQ-GDNSQVLOLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRV 238

DB 111 NAKDEQWTLHFHFAAQNGDESSTRLLLEKN--ASVNEVDTEGRTPMHVACQHQENIVRI 168

QY 239 LLLCNARCNIMPGY-PIHSAMKFSQKGCACMIISMDSQIHSKDPYRGASPLHWAK-- 295

DB 169 LLRRGVDSVLOGKDAWLPVHYAAWQGHLPVVKLLAKQPGVSVNAQ-TLDGRTPLHLAQR 227

QY 296 -NAEMARMLKRCNVNSTSSAGNTALHVGVMNRNFDCAIVLTHGANADARGEHNTPL 354

DB 228 GHYRVARILIDLCSQVNVCSLLAQTPHVAARETGTSTARLLHLHRGAGKEAVTSDGYTAL 287

QY 355 HLMSKDNVEMIKALIVFGAEVDTNDFGCTPTFLASKIG 394

DB 288 HLAARNGHLATVKLLIVEEKADVLARGPLNQTLALHAAAAG 327

Search completed: May 26, 2005, 14:20:31

Job time : 14.279 secs

QY 240 LLCNARCNTMGPNY-PIHSAMKFSQKGAEMIISMDSQIHSKDPKYGASPLHWA---K 295
Db 535 LDHGASLSITTKGFTPLHVAKYGKLEVASLLLOKSASP--DAACKSGLTPLHVAHYD 592
QY 296 NAEMARMMLKRCGNVNSTSAGNTALHVGVMNRFPDCAIVLLTHGANADARGEHGNTPHL 355
Db 593 NOKVALLLDQGSAPHAANKGYTPPLHIAAKKNQMDIATSLLEYGADANAVTRQGIASVH 652
QY 356 LAMSKDNVEMIKALIVFGAEVDTPNDFGETPTFLASK 392
Db 653 LAAQEGHVDVMSLLSRNANVLSNKSGLTPLHAAQ 689
RESULT 12
T42716
ankyrin 3, splice form 4 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42716
R:Peterson, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, J.
J. Cell Biol. 130, 313-330, 1995
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A:Reference number: Z22237; MUID:95340633; PMID:7615634
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Accession: T42716
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1961 <P>
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710552; PIDN:AA801607
A:Experimental source: strain C57BL/6J; kidney
C:Genetics:
A:Gene: Ank3
A:Map position: 10
A:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
Query Match 14.1%; Score 293; DB 2; Length 1961;
Best Local Similarity 29.2%; Pred. No. 3.9e-16;
Matches 81; Conservative 55; Mismatches 125; Indels 16; Gaps 7;
QY 124 HLAVELG----TRECFFHRIISCANCAENEGCTPLHLACRKGDEIIVELVQYCHTQM 179
Db 421 HVAAFMGHNVISQLMH-----GASPTNTNVRGETALHVAARSQGAEEVVRVYLQ-DGAQV 475
QY 180 DVTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNOGLTPLHLACQLGQKQEMVRVL 239
Db 476 EAKAKDDQPLHISARIGKADIVQQLQOG-ASPNAATTSGYTPPLHAAAREGHEDVA AFL 534
QY 240 LLCNARCNTMGPNY-PIHSAMKFSQKGAEMIISMDSQIHSKDPKYGASPLHWA---K 295
Db 535 LDHGASLSITTKGFTPLHVAKYGKLEVASLLLOKSASP--DAACKSGLTPLHVAHYD 592
QY 296 NAEMARMMLKRCGNVNSTSAGNTALHVGVMNRFPDCAIVLLTHGANADARGEHGNTPHL 355
Db 593 NOKVALLLDQGSAPHAANKGYTPPLHIAAKKNQMDIATSLLEYGADANAVTRQGIASVH 652
QY 356 LAMSKDNVEMIKALIVFGAEVDTPNDFGETPTFLASK 392
Db 653 LAAQEGHVDVMSLLSRNANVLSNKSGLTPLHAAQ 689
RESULT 13
S3771
ankyrin, erythrocyte - mouse
C:Species: Mus musculus (house mouse)
C>Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: S3771
R:Birkenmeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.
J. Biol. Chem. 268, 9533-9540, 1993
A:Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found am
A:Reference number: S3771; MUID:93252825; PMID:8486643
A:Accession: S3771
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-1848

A:Cross-references: UNIPROT:Q61302; EMBL:X69063; NID:g311816; PIDN:CAA48801.1; PID:g31181
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
F:48-80/Domain: ankyrin repeat homology <AN01>
F:91-113/Domain: ankyrin repeat homology <AN02>
F:114-146/Domain: ankyrin repeat homology <AN03>
F:147-175/Domain: ankyrin repeat homology <AN04>
F:176-208/Domain: ankyrin repeat homology <AN05>
F:209-241/Domain: ankyrin repeat homology <AN06>
F:242-274/Domain: ankyrin repeat homology <AN07>
F:275-307/Domain: ankyrin repeat homology <AN08>
F:308-340/Domain: ankyrin repeat homology <AN09>
F:341-373/Domain: ankyrin repeat homology <AN10>
F:374-406/Domain: ankyrin repeat homology <AN11>
F:407-439/Domain: ankyrin repeat homology <AN12>
F:440-472/Domain: ankyrin repeat homology <AN13>
F:473-505/Domain: ankyrin repeat homology <AN14>
F:506-538/Domain: ankyrin repeat homology <AN15>
F:539-571/Domain: ankyrin repeat homology <AN16>
F:572-604/Domain: ankyrin repeat homology <AN17>
F:605-637/Domain: ankyrin repeat homology <AN18>
F:638-670/Domain: ankyrin repeat homology <AN19>
F:671-703/Domain: ankyrin repeat homology <AN20>
F:704-736/Domain: ankyrin repeat homology <AN21>
F:737-769/Domain: ankyrin repeat homology <AN22>
F:770-802/Domain: ankyrin repeat homology <AN23>
Query Match 13.7%; Score 285; DB 2; Length 1848;
Best Local Similarity 25.6%; Pred. No. 1.7e-15;
Matches 93; Conservative 55; Mismatches 121; Indels 94; Gaps 10;
QY 107 LOHLDLIRNHPFSVAHLAVELGIRECFHH--SRIISCANCAENE---EGCTPLHLACR 161
Db 340 LDHLTPL-----HVAA-----HCGHHRVAKVLLDKGAKPNSRALNGFTPLHIACK 384
QY 162 KGDGEILVELVQYCHTQMD-----VTDYKGET 188
Db 385 KKHIRVM-ELLKTKGASIDAVTESGLTPLHVASFMGHLPIVKNLLQORGASPNVSNKVET 443
QY 189 VFHYAVQGDNSQVLLGRNAVAGLNQVNOGLTPLHLACQLGQKQEMVRVLLCNARCNI 248
Db 444 PLHMAARAGHTEVAKYLLQNK-AKANAKAKDDQTPHLCAARIGHTGWVLLLENGASPNL 502
QY 249 MGPNGY-----PIHSAMKFSQKGAEMIISM 274
Db 503 ATTAGHTPLHTAAREGHVDTALALLEKEASQACMTKKGFTPLHVAAYKGVRLAELEH 562
QY 275 DSSQIHSKDPKYGASPLHWA---KNAEMARMMLKRCGNVNSTSAGNTALHVGVMNRFD 331
Db 563 DAHP--NAACKNGLTPLHVAHVHNNLDIVKLLLPGRGSPHSPAWNGYTPPLHIAAKQNOIE 620
QY 332 CAIVLLTHGANADARGEHGNTPPLHLAMSKDNVEMIKALIVFGAEVDTPNDFGETPTFLAS 391
Db 621 VARSLLQYGSANAESVQGVTPPLHAAQEGHTEWVALLLSKQANGNLGNKSGLTPLHLVS 680
QY 392 KIG 394
Db 681 QEG 683
RESULT 14
I49502
ankyrin - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49502
R:White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.
Mamm. Genome 3, 281-285, 1992
A:Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory doma
A:Reference number: I49502; MUID:92345717; PMID:1386265
A:Accession: I49502

Qy	332	CAIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTPNDGETPTFFLAS	391
		: : : :	
Db	617	VARSLLQYGGSSANAESVQGVTPHLAAQEGHAEMVALLLSKQANGNLGNKSGLTPHLVA	676
Qy	392	KIG	394
		:	
Db	677	OBG	679

RESULT 9
T42714
ankyrin 3, splice form 2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42714
R:Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
J. Cell Biol. 130, 313-330, 1995
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A:Reference number: Z22337; MUID:95340633; PMID:7615634
A:Accession: T42714
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1765 <P>
A:Cross-references: UNIPROT:Q61307; EMBL:U40632; NID:G710548; PID:G710551; PIDN:AAB01605
A:Experimental source: strain C57BL/6J; kidney
C:Genetics:
A:Gene: Ank3
A:Map position: 10
A:Introns: 1587/1
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing

Query Match	14.1%	Score 293;	DB 2;	Length 1765;
Best Local Similarity	29.2%;	Pred. No. 3.4e-16;		
Matches	81;	Conservative 55;	Mismatches 125;	Indels 16; Gaps 7;
Qy	124	HLAVELG----	IRCFHHSRIISCANCAENBEGCTPLHLACRKGDGELVELVQYCHTQM	179
Db	421	HVAAFMGHVNIVS	QLMHH---GASPTNTNVRGETALHMAARSGOAEVRYLVQ--DGAQV	475
Qy	180	DVTDYKGETVFHYAVQGDNSOV	LQLLGNVAVAGLNVQNNQGLTPLHLACQLGKQEMVRVL	239
Db	476	EAKAKDQDTPLHISARLGKADIV	QOOLQQG--ASPNAATTSGYTPFLHLAAREGHEDVA AFL	534
Qy	240	LLCNARCNIMGPNGY--PIHSAMKFS	QKGC AEMII SMDOSSQHSKDPYRGASPLHWA---K	295
Db	535	LDHGASLSITTTKKGFTPLHVA	AKYKLEVASLLQLKSGASP--DAAGKSGLTPLHVA AHYD	592
Qy	296	NAENARMILLKRCNCVNSTSS	AGNTALHVGVMRNFDCAI VLLTHGANADARGEHNTPLH	355
Db	593	NQKVALLLLDQASPHAAAKNGY	TPFLHIAAKNQMDIATSLLEYGADANAVTROGIA SVH	652
Qy	356	LAMSKDNVEMIKALIVFGAEV	DTNPDEFGETPTFLASK	392
Db	653	LAAOEGHVDWVSLLLSRNANV	LSNKNKSGLTPLHLAAO	689

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RESULT 10
T42715
  ankyrin 3, splice form 3 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42715
R:Peter, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I.
  J. Cell Biol. 130, 313-330, 1995
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
  the repeat domain.
A:Reference number: Z22237; MUID:95340633; PMID:7615634
A:Accession: T42715
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1940 <PET>

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A: Cross-references: UNIPROT:Q61307; EMBL:U40632; NID:g710549; PID:g710548; NID:g710549; PID:g710549; PIDN:AA016014

Query Match	14.1%;	Score 293;	DB 2;	Length 1940;
Best Local Similarity	29.2%;	Pred. No. 3.8e-16;		
Matches	81;	Conservative 55;	Mismatches 125;	Indels 16; Gaps 7;
Qy	124	HLAVELG----	IRCFHHSRIISCANCAENEGCITPLHLACRKGDEILLVELVQYCHTQM	179
Db	421	HVAAFMGHVNTIVSQMHH----	GASPTNTNVRGETALHWAARSGQAEVVRVLYQV-DGAQV	475
Qy	180	DVTDYKGETVPHYAVOGDNSOVLQLLGRNAVAGLNQVNNQGLTPLHLACOLGQGMVRVL	239	
Db	476	EAKAKDDTPLHISARLGKADIVQQLQOG-ASPNAATTSGYTPPLHLAAREGHEDVA AFL	534	
Qy	240	LLCNARCNIMGPGY-PHISAMKFQKQCAEMIISMSSQIHSKDPYRGASPLHWA---	K 295	
Db	535	LDHGASLSITTKGETPLHVAAKYKLEVASLLLOKSASP--DAACKSGITPLHVAHYD	592	
Qy	296	NAEMARMLLKRCGNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGHBGNTPLH	355	
Db	593	NOKVALLLLDQASPHAAAKNGYTPPLHIAAKKNQMDIATSLLEYGADANAVTRQGIASVH	652	
Qy	356	LAMSKDNVEMITKALIVFGAEVDTPNDFGETPTFLASK	392	
Db	653	LAAQEGHYDVMVSLLSIRNANVNLNSKSGITPLHLAAQ	689	

RESULT 11

T42713
ankyrin 3, splice form 1 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C/Accession: T42713
R;Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
J. Cell Biol. 130, 313-330, 1995
A>Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A/Reference number: Z22237; MUID:95340633; PMID:7615634
A/Accession: T42713
A>Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1943 <PPT>
A/Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710550; PIDN:AA01606
A/Experimental source: strain C57BL/6J; kidney
C/Genetics:
A/Gene: Ank3
A/Map position: 10
A/Introns: 855/1
C/Function:
A/Description: supposed to play an important role in the polarized distribution of many
A/Note: major kidney ankyrin
C/Superfamily: ankyrin; ankyrin repeat homology
C/Keywords: alternative splicing

	Query Match	14.1%;	Score 293;	DB 2;	Length 1943;
	Best Local Similarity	29.2%;	Pred. No. 3.8e-16;		
	Matches	81;	Conservative 55;	Mismatches 125;	Indels 16; Gaps 7;
Qy	124	HLAVELG---IRECFHRSRIISCANCAENEEGCTPLHLACRGDGEILVELVQYCHQM	179		
	..	: :	:	:	:
	:	:	:	:	:
Dd	421	HVAAPMGHNIVSQLMHH-----GASPTTNRGETALEHMAARSGQAEVVRYLVQ-DGAQV	475		
	..	: :	:	:	:
	:	:	:	:	:
Qy	180	DVTDYKGTTFHYAQQDNSSQVLQLLGRNAVAGLNQNNOCGLTPHLHLACOLGKQEMRVYL	239		
	..	: :	:	:	:
	:	:	:	:	:
Dd	476	EAKAKDDQTPLHISARLGKADIVQQLLOQG-ASPNAATTSGYTPLHLAAAREGHEDVA AFL	534		
	..	: :	:	:	:
	:	:	:	:	:

F:597-629/Domain: ankyrin repeat homology <AN17> F:630-662/Domain: ankyrin repeat homology <AN18> F:663-695/Domain: ankyrin repeat homology <AN19> F:696-728/Domain: ankyrin repeat homology <AN20> F:729-761/Domain: ankyrin repeat homology <AN21> F:762-794/Domain: ankyrin repeat homology <AN22> F:795-827/Domain: ankyrin repeat homology <AN23>	Query Match 14.2%; Score 296; DB 2; Length 4377; Best Local Similarity 29.2%; Pred. No. 6.5e-16; Matches 81; Conservative 54; Mismatches 130; Indels 12; Gaps 6;	
QY 124 HLAVALGIRECFHRSRIISCANCAENESGCTPLHLACRKGDEILVELVOYCHTOMDVTD 183 DB 504 HISARLKGADIVQQLQOGASNAATTSGYTPHLISAREGHEDVAFLLDH-GASLSITT 562		
QY 184 YKGETVFHVAVQDINSQVLQGLGRNAVAGLNQVNOGLTPLHLACOLGQKQEMVRVLLCN 243 DB 563 KGFTPLHVAAYKYGKLEVANLLQKS-ASPDAGKSGLTPLHVAHYDNQKVALLLDQ 621		
QY 244 ARCNTMGPNY-PIHSAMKFSQKGAEMII--SMDSQIHSKDPYRGASPLHWAK---NA 297 DB 622 ASPHAAKNGYTPHLIAAKNQMDIATTLLEYGADANAV---TRQGIASVHLAAQEGHV 677		
QY 298 ENARMILLKGCNNVSTSSAGNTALHVGWVRNRPDCAIVLLTHGANADARGEHGTPLHLA 357 DB 678 DMVSLGRNANVNLNKGSLTPLHLAAQEDRVNVAEVLVNGAHVDAQTRMGYTPLVHG 737		
QY 358 NSKDNVEMKALIVGAEDVTENDFGETPTFLASKIG 394 DB 738 CHYGNIKIIVNLFQHSKAKVNAKTNGYTPHLHQAQOG 774		
RESULT 6 B35049 Ankyrin 1, erythrocyte splice form 3 - human N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R N:Contains: ankyrin 2.2, erythrocyte C:Species: Homo sapiens (man) C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998 C:Accession: B35049 R:Lambert, S.; Yu, H.; Prochal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990 A:Title: cDNA sequence for human erythrocyte ankyrin. A:Reference number: A35049; MUID:90175370; PMID:1689849 A:Accession: B35049 A:Status: preliminary A:Molecule type: mRNA A:Residues: 1-1856 <LAM> C:Genetics: A:Gene: GDB:ANK1; ANK A:Cross-references: GDB:118737; OMIM:182900 A:Map position: 8p11.2-8p11.2 A:Superfamily: ankyrin; ankyrin repeat homology C:Keywords: alternative splicing F:2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT> F:2-1513.1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2> F:44-76/Domain: ankyrin repeat homology <AN01> F:77-109/Domain: ankyrin repeat homology <AN02> F:110-142/Domain: ankyrin repeat homology <AN03> F:143-171/Domain: ankyrin repeat homology <AN04> F:172-204/Domain: ankyrin repeat homology <AN05> F:205-237/Domain: ankyrin repeat homology <AN06> F:238-270/Domain: ankyrin repeat homology <AN07> F:271-303/Domain: ankyrin repeat homology <AN08> F:304-336/Domain: ankyrin repeat homology <AN09> F:337-369/Domain: ankyrin repeat homology <AN10> F:370-402/Domain: ankyrin repeat homology <AN11> F:403-435/Domain: ankyrin repeat homology <AN12> F:436-468/Domain: ankyrin repeat homology <AN13> F:469-501/Domain: ankyrin repeat homology <AN14> F:502-534/Domain: ankyrin repeat homology <AN15> F:535-567/Domain: ankyrin repeat homology <AN16>		
F:568-600/Domain: ankyrin repeat homology <AN17> F:601-633/Domain: ankyrin repeat homology <AN18> F:634-666/Domain: ankyrin repeat homology <AN19> F:667-699/Domain: ankyrin repeat homology <AN20> F:700-732/Domain: ankyrin repeat homology <AN21> F:733-765/Domain: ankyrin repeat homology <AN22> F:766-798/Domain: ankyrin repeat homology <AN23>	Query Match 14.1%; Score 294; DB 2; Length 1856; Best Local Similarity 25.6%; Pred. No. 3e-16; Matches 93; Conservative 57; Mismatches 119; Indels 94; Gaps 10;	
QY 107 LQHLTDLIRNHPSSVAHLAVELGIRECFH--SRIISCANCAENE---EGCTPLHLACR 161 DB 336 LDHLTPL-----HVAA-----HCGHHRVAKVLLDKGAKPNSRALNGFTPLHIACK 380		
QY 162 KGDGEILVELVOYCHTOMD-----VTDYKGET 188 DB 381 KNHVRVM-ELLKTKASIDAVTESGLTPLHVASFMGHLPIVKNLLQRGASPNVSNVKVET 439		
QY 189 VFHVAVQDINSQVLQGLGRNAVAGLNQVNOGLTPLHLACOLGQKQEMVRVLLCNARCM 248 DB 440 PLHMAARAGHTEVAKYLLQNK-AKYNAKAKDDQTPHLHCAARIGHTNMVKLLLENNANPUL 498		
QY 249 MGPNGY-----PIHSAMKFSQKGAEMIIISM 274 DB 499 ATTAGTPLHIAAREGHVETVLALLEKEASQACMTKGFTPLHVAAYKYGKVRVALLER 558		
QY 275 DSSQIHSKDPYRGASPLHWA---KNAEMARMILLKGCNNVSTSSAGNTALHVGWVRNRPD 331 DB 559 DAHP--NAAKNGLTPLHVAHVHNNLDIVKLLPRGSGSPHSPAWNNGYTPHLHAAKQNOVE 616		
QY 332 CAIVLLTHGANADARGEHGTPLHLAMSNDVEMKALIVFGAEVDTNDPFGETPTFLAS 391 DB 617 VARSLLQYGGSSANAESVQGVTPHLAAQEGHAEVALLSKQANGNLGKSLTPLHLVA 676		
QY 392 KIG 394 DB 677 QEG 679		
RESULT 7 B35049 Ankyrin 1, erythrocyte splice form 2 - human N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R N:Contains: ankyrin 2.2, erythrocyte C:Species: Homo sapiens (man) C:Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 09-Jul-2004 C:Accession: A35049 R:Lambert, S.; Yu, H.; Prochal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990 A:Title: cDNA sequence for human erythrocyte ankyrin. A:Reference number: A35049; MUID:90175370; PMID:1689849 A:Accession: A35049 A:Status: preliminary A:Molecule type: mRNA A:Residues: 1-1880 <LAM> A:Cross-references: UNIPROT:P16157; GB:M28880 C:Genetics: A:Gene: GDB:ANK1; ANK A:Cross-references: GDB:118737; OMIM:182900 A:Map position: 8p11.2-8p11.2 A:Superfamily: ankyrin; ankyrin repeat homology C:Keywords: alternative splicing; cytoskeleton F:2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAT> F:2-1513.1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA2> F:44-76/Domain: ankyrin repeat homology <AN01> F:77-109/Domain: ankyrin repeat homology <AN02> F:110-142/Domain: ankyrin repeat homology <AN03> F:143-171/Domain: ankyrin repeat homology <AN04> F:172-204/Domain: ankyrin repeat homology <AN05> F:205-237/Domain: ankyrin repeat homology <AN06> F:238-270/Domain: ankyrin repeat homology <AN07>		

A>Title: An ankyrin-related gene (unc-44) is necessary for proper axonal guidance in Cae
A:Reference number: A57282; MUID:95263663; PMID:7744957
A:Accession: A57282
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-852; GGG, 856-1000, 'SKLOHRT', 1002-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEH', 'SHRED', 2007-2008, 'TI', 2011, 2017, 'TT', 2020-2022, 'SHIS', <OTS>
A:Cross-references: GB:U21734; NID:g790607; PIDN:AAA85854.1; PID:g790608
A:Accession: B57282
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 831-852, 'GGG', 856-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEHNLRL', 1727, 1799, 'H', 1945-1947, 'VT', 1950, 'SH', 1975, 'SESP', 1980-1981, 'SPTRRSVEPEERHS', 1984-1985, 'EDHEGS', 1988-1990, 'V', 1994-1995, 'V', 1998-1999, 'V', 2000-2001, 'V', 2002-2003, 'V', 2004-2005, 'V', 2006-2007, 'V', 2008-2009, 'V', 2010-2011, 'V', 2012-2013, 'V', 2014-2015, 'V', 2016-2017, 'V', 2018-2019, 'V', 2020-2021, 'V', 2022-2023, 'V', 2024-2025, 'V', 2026-2027, 'V', 2028-2029, 'V', 2030-2031, 'V', 2032-2033, 'V', 2034-2035, 'V', 2036-2037, 'V', 2038-2039, 'V', 2040-2041, 'V', 2042-2043, 'V', 2044-2045, 'V', 2046-2047, 'V', 2048-2049, 'V', 2050-2051, 'V', 2052-2053, 'V', 2054-2055, 'V', 2056-2057, 'V', 2058-2059, 'V', 2060-2061, 'V', 2062-2063, 'V', 2064-2065, 'V', 2066-2067, 'V', 2068-2069, 'V', 2070-2071, 'V', 2072-2073, 'V', 2074-2075, 'V', 2076-2077, 'V', 2078-2079, 'V', 2080-2081, 'V', 2082-2083, 'V', 2084-2085, 'V', 2086-2087, 'V', 2088-2089, 'V', 2090-2091, 'V', 2092-2093, 'V', 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S37431
ankyrin 2, neuronal long splice form - human
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C:Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 09-Jul-2004
C:Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569
R:Chan, W.
submitted to the EMBL Data Library, September 1993
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R:Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.
J. Cell Biol. 114, 241-253, 1991
A:Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal a
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A:Cross-references: EMBL:X56958
R:Tse, W.T.; Wenzinger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Ward, H.
Genomics 10, 858-866, 1991
A:Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.
A:Reference number: A40334; MUID:92009921; PMID:1833308
A:Accession: A40334
A:Molecule type: DNA
A:Residues: 463-474, 'PE', 477-495 <TSE>
A:Cross-references: GB:M37123; NID:G178647; PIDN:AAA62828.1; PID:G178648
R:Chan, W.; Kordeli, E.; Bennett, V.
J. Cell Biol. 123, 1463-1473, 1993
A:Title: 440-kD ankyrinB: structure of the major developmentally regulated domain and sequence
A:Reference number: A49462; MUID:94075409; PMID:8253844
A:Accession: A49462
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-3924 <RES>
A:Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288
C:Genetics:
A:Gene: GDB:ANK2
A:Cross-references: GDB:127607; OMIM:106410
A:Map position: 4q25-4q27
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
F:2-3924/Product: ankyrin 2, long form #status predicted <MAT>
F:2-1443,3585-3924/Product: ankyrin 2, short form #status predicted <MA2>
F:63-95/Domain: ankyrin repeat homology <AN01>
F:96-128/Domain: ankyrin repeat homology <AN02>
F:129-161/Domain: ankyrin repeat homology <AN03>
F:162-190/Domain: ankyrin repeat homology <AN04>
F:191-223/Domain: ankyrin repeat homology <AN05>
F:232-264/Domain: ankyrin repeat homology <AN06>
F:265-297/Domain: ankyrin repeat homology <AN07>
F:298-330/Domain: ankyrin repeat homology <AN08>
F:331-363/Domain: ankyrin repeat homology <AN09>
F:364-396/Domain: ankyrin repeat homology <AN10>
F:397-429/Domain: ankyrin repeat homology <AN11>
F:430-462/Domain: ankyrin repeat homology <AN12>
F:463-495/Domain: ankyrin repeat homology <AN13>
F:496-528/Domain: ankyrin repeat homology <AN14>
F:529-561/Domain: ankyrin repeat homology <AN15>
F:562-594/Domain: ankyrin repeat homology <AN16>
F:595-627/Domain: ankyrin repeat homology <AN17>
F:628-660/Domain: ankyrin repeat homology <AN18>
F:661-693/Domain: ankyrin repeat homology <AN19>

F;694-726/Domain: ankyrin repeat homology <AN20>
F;727-759/Domain: ankyrin repeat homology <AN21>
F;760-792/Domain: ankyrin repeat homology <AN22>
F;793-825/Domain: ankyrin repeat homology <AN23>

Query Match 15.9%; Score 332; DB 2; Length 3924;
Best Local Similarity 27.3%; Pred. No. 4.8e-19;
Matches 100; Conservative 62; Mismatches 127; Indels 77; Gaps 9;

Qy 103 HTEVLQHLT-----LIRNHPSPSWAHLAVELGIRECFHH-----SRII 141
Db 311 HDQVVELLGGAPLAAATKNGLSPLHMAAQGDHVECVKHLLOHKAPVDDVTLDTLALH 370
Qy 142 SCANC-----AENEEGCTPLHLACRKGDEILVELVOY----- 174
Db 371 VAACHGHYRVTKLLLDKRANPNARALNGFTPLHIAACKNKRIKVMELLVKYASIQAITES 430
Qy 175 -----CH-----TQMDVTDYKGETVFHYAVQGDNSQVLQLGRNAVAG 212
Db 431 GLTPIHVAAFMGLHNLVILLLLQNGASPDVTNRTGRTALHMAARAGQVEVVRCLLRNG-AL 489
Qy 213 LQNVNNOGLTPLHLACOLGKQEMVRLVLLLCNARCINIMGPNGY-PIHSAMKFSOKGCAEMI 271
Db 490 VDAARAEQTPPLHRSRGLKTEIVOLLQMAHPDRAATNGYTPPLHISAREGQVDVASVL 549
Qy 272 ISMSSQIHSKDPRYGASPLHWAK---NAEMARMLLKRCNCVNINSTSAGNTALHVGVMRN 328
Db 550 --LEAGAAHSLATKGGFTPLHVAAYGSLDVAKLLQRRAAADSAGKNGGLTPLHVAAHYD 607
Qy 329 RFDCAVLLTGANADARGEHNTPLHLAMSKONVEMIKALIVFGAEVTPNDFGETPTTF 388
Db 608 NQKVALLLLEKGGASHATAKNGYTPPLHIAAKKNQMQIASTLLNNGAETNIVTRQGVTPH 667
Qy 389 LASKIG 394
Db 668 LASQEG 673

RESULT 3
T15347
ankyrim-related unc-44 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence revision 20-Sep-1999 #text change 09-Jul-2004
C;Accession: T15347; T15346; T15344; T15345; A57282; B57282; C57282
R;Gattung, S.
submitted to the EMBL Data Library, February 1996
A;Description: The sequence of C. elegans cosmid B0350.
A;Reference number: Z18332
A;Accession: T15347
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2039 <GAT>
A;Cross-references: UNIPROT:Q17489; EMBL:U50071; NID:g1208871; PID:g1208873; PIDN:AAA93444.1
A;Accession: T15346
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1000, 'SKLQHRT', 1002-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVAES', 1956-1957, 'EQVPE', 1958-1959, 'PSPQR', 1960-1961, 'PSPQR', 1962-1963, 'PSPQR', 1964-1965, 'PSPQR', 1966-1967, 'PSPQR', 1968-1969, 'PSPQR', 1970-1971, 'PSPQR', 1972-1973, 'PSPQR', 1974-1975, 'PSPQR', 1976-1977, 'PSPQR', 1978-1979, 'PSPQR', 1980-1981, 'PSPQR', 1982-1983, 'PSPQR', 1984-1985, 'PSPQR', 1986-1987, 'PSPQR', 1988-1989, 'PSPQR', 1990-1991, 'PSPQR', 1992-1993, 'PSPQR', 1994-1995, 'PSPQR', 1996-1997, 'PSPQR', 1998-1999, 'PSPQR', 2000-2001, 'PSPQR', 2002-2003, 'PSPQR', 2004-2005, 'PSPQR', 2006-2007, 'PSPQR', 2008-2009, 'PSPQR', 2010-2011, 'PSPQR', 2012-2013, 'PSPQR', 2014-2015, 'PSPQR', 2016-2017, 'PSPQR', 2018-2019, 'PSPQR', 2020-2021, 'PSPQR', 2022-2023, 'PSPQR', 2024-2025, 'PSPQR', 2026-2027, 'PSPQR', 2028-2029, 'PSPQR', 2030-2031, 'PSPQR', 2032-2033, 'PSPQR', 2034-2035, 'PSPQR', 2036-2037, 'PSPQR', 2038-2039, 'PSPQR', 2040-2041, 'PSPQR', 2042-2043, 'PSPQR', 2044-2045, 'PSPQR', 2046-2047, 'PSPQR', 2048-2049, 'PSPQR', 2050-2051, 'PSPQR', 2052-2053, 'PSPQR', 2054-2055, 'PSPQR', 2056-2057, 'PSPQR', 2058-2059, 'PSPQR', 2060-2061, 'PSPQR', 2062-2063, 'PSPQR', 2064-2065, 'PSPQR', 2066-2067, 'PSPQR', 2068-2069, 'PSPQR', 2070-2071, 'PSPQR', 2072-2073, 'PSPQR', 2074-2075, 'PSPQR', 2076-2077, 'PSPQR', 2078-2079, 'PSPQR', 2080-2081, 'PSPQR', 2082-2083, 'PSPQR', 2084-2085, 'PSPQR', 2086-2087, 'PSPQR', 2088-2089, 'PSPQR', 2090-2091, 'PSPQR', 2092-2093, 'PSPQR', 2094-2095, 'PSPQR', 2096-2097, 'PSPQR', 2098-2099, 'PSPQR', 2100-2101, 'PSPQR', 2102-2103, 'PSPQR', 2104-2105, 'PSPQR', 2106-2107, 'PSPQR', 2108-2109, 'PSPQR', 2110-2111, 'PSPQR', 2112-2113, 'PSPQR', 2114-2115, 'PSPQR', 2116-2117, 'PSPQR', 2118-2119, 'PSPQR', 2120-2121, 'PSPQR', 2122-2123, 'PSPQR', 2124-2125, 'PSPQR', 2126-2127, 'PSPQR', 2128-2129, 'PSPQR', 2130-2131, 'PSPQR', 2132-2133, 'PSPQR', 2134-2135, 'PSPQR', 2136-2137, 'PSPQR', 2138-2139, 'PSPQR', 2140-2141, 'PSPQR', 2142-2143, 'PSPQR', 2144-2145, 'PSPQR', 2146-2147, 'PSPQR', 2148-2149, 'PSPQR', 2150-2151, 'PSPQR', 2152-2153, 'PSPQR', 2154-2155, 'PSPQR', 2156-2157, 'PSPQR', 2158-2159, 'PSPQR', 2160-2161, 'PSPQR', 2162-2163, 'PSPQR', 2164-2165, 'PSPQR', 2166-2167, 'PSPQR', 2168-2169, 'PSPQR', 2170-2171, 'PSPQR', 2172-2173, 'PSPQR', 2174-2175, 'PSPQR', 2176-2177, 'PSPQR', 2178-2179, 'PSPQR', 2180-2181, 'PSPQR', 2182-2183, 'PSPQR', 2184-2185, 'PSPQR', 2186-2187, 'PSPQR', 2188-2189, 'PSPQR', 2190-2191, 'PSPQR', 2192-2193, 'PSPQR', 2194-2195, 'PSPQR', 2196-2197, 'PSPQR', 2198-2199, 'PSPQR', 2200-2201, 'PSPQR', 2202-2203, 'PSPQR', 2204-2205, 'PSPQR', 2206-2207, 'PSPQR', 2208-2209, 'PSPQR', 2210-2211, 'PSPQR', 2212-2213, 'PSPQR', 2214-2215, 'PSPQR', 2216-2217, 'PSPQR', 2218-2219, 'PSPQR', 2220-2221, 'PSPQR', 2222-2223, 'PSPQR', 2224-2225, 'PSPQR', 2226-2227, 'PSPQR', 2228-2229, 'PSPQR', 2230-2231, 'PSPQR', 2232-2233, 'PSPQR', 2234-2235, 'PSPQR', 2236-2237, 'PSPQR', 2238-2239, 'PSPQR', 2240-2241, 'PSPQR', 2242-2243, 'PSPQR', 2244-2245, 'PSPQR', 2246-2247, 'PSPQR', 2248-2249, 'PSPQR', 2250-2251, 'PSPQR', 2252-2253, 'PSPQR', 2254-2255, 'PSPQR', 2256-2257, 'PSPQR', 2258-2259, 'PSPQR', 2260-2261, 'PSPQR', 2262-2263, 'PSPQR', 2264-2265, 'PSPQR', 2266-2267, 'PSPQR', 2268-2269, 'PSPQR', 2270-2271, 'PSPQR', 2272-2273, 'PSPQR', 2274-2275, 'PSPQR', 2276-2277, 'PSPQR', 2278-2279, 'PSPQR', 2280-2281, 'PSPQR', 2282-2283, 'PSPQR', 2284-2285, 'PSPQR', 2286-2287, 'PSPQR', 2288-2289, 'PSPQR', 2290-2291, 'PSPQR', 2292-2293, 'PSPQR', 2294-2295, 'PSPQR', 2296-2297, 'PSPQR', 2298-2299, 'PSPQR', 2300-2301, 'PSPQR', 2302-2303, 'PSPQR', 2304-2305, 'PSPQR', 2306-2307, 'PSPQR', 2308-2309, 'PSPQR', 2310-2311, 'PSPQR', 2312-2313, 'PSPQR', 2314-2315, 'PSPQR', 2316-2317, 'PSPQR', 2318-2319, 'PSPQR', 2320-2321, 'PSPQR',

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:07:29 ; Search time 11.279 Seconds
(without alignments)
3361.064 Million cell updates/sec

Title: US-10-612-668-17

Perfect score: 2084
Sequence: 1 MQFFGLVNTFSGVTNLFNS.....EVDTPNDFGETPTFLASKIG 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2078	99.7	851	T12503	hypothetical prote
2	332	15.9	3924	S37431	ankyrin 2, neurona
3	318	15.3	2039	T15347	ankyrin-related un
4	313.5	15.0	1549	T13940	ankyrin - fruit fl
5	296	14.2	4377	A55575	ankyrin 3, long sp
6	294	14.1	1856	B35049	ankyrin 1, erythro
7	294	14.1	1880	A35049	ankyrin 1, erythro
8	294	14.1	1881	SJRHUK	ankyrin 1, erythro
9	293	14.1	1765	T42714	ankyrin 3, splice
10	293	14.1	1940	T42715	ankyrin 3, splice
11	293	14.1	1943	T42713	ankyrin 3, splice
12	293	14.1	1961	T42716	ankyrin 3, splice
13	285	13.7	1848	S37771	ankyrin, erythrocy
14	285	13.7	1862	T49502	ankyrin - mouse
15	281.5	13.5	397	T46445	hypothetical prote
16	258	12.4	1023	T26261	hypothetical prote
17	255.5	12.3	1411	S30355	alpha-latroinsecto
18	249	11.9	791	T42691	hypothetical prote
19	248.5	11.9	1435	T32930	hypothetical prote
20	244	11.7	247	D84448	probable ankyrin l
21	237	11.3	1401	T11527	alpha-latrotoxin p
22	236	11.3	2437	S42612	transmembrane prot
23	234	11.2	1423	T37275	death-associated p
24	233	11.2	426	A82149	hypothetical prote
25	231	11.1	934	H71274	probable ankyrin
26	225	10.8	1071	T22327	hypothetical prote
27	218.5	10.5	368	T18184	ankyrin repeat pro
28	216.5	10.4	633	T27499	hypothetical prote
29	216.5	10.4	1184	T00253	gene Ankhzn protei

RESULT 2

ALIGNMENTS

RESULT 1

T12503
hypothetical protein DKFP434A102.1 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C:Accession: T12503
R:Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z17527
A:Accession: T12503
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-851 <ANS>
A:Cross-references: EMBL:AL080187
A:Experimental source: adult testis; clone DKFP434A102
C:Genetics:
A>Note: DKFP434A102.1

Query Match 99.7%; Score 2078; DB 2; Length 851;
Best Local Similarity 99.7%; Pred. No. 1.6e-168;
Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MOFFGLVNTFSGVTNLFNSNPRFRKEVAVADYTSRVRREGQLILFQNTPNRTWDCVLV	60
DB	46	MOFFGLVNTFSGVTNLFNSNPRFRKEVAVADYTSRVRREGQLILFQNTPNRTWDCVLV	105
QY	61	NPRNSQSGFRLFQLEADALVNFHOYSQQLLPFYESSQVLTHTVLQHLTDLIRNHPWS	120
DB	106	NPRNSQSGFRLFQLEADALVNFHOYSQQLLPFYESSQVLTHTVLQHLTDLIRNHPWS	165
QY	121	SVNHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDGELVELVOYCHTQMD	180
DB	166	SVNHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDGELVELVOYCHTQMD	225
QY	181	VDYKGETVFHVAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL	240
DB	226	VDYKGETVFHVAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL	285
QY	241	LCNARCNIIMPNGYPITHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHWAKNAEMA	300
DB	286	LCNARCNIIMPNGYPITHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHWAKNAEMA	345
QY	301	RMLLKGCNNVNTSSAGNTALHVGUNRNFDCAIVLTHGCANADARGEHGTPLHLAMSK	360
DB	346	RMLLKGCNNVNTSSAGNTALHVGUNRNFDCAIVLTHGCANADARGEHGTPLHLAMSK	405
QY	361	DNVEMIKALIVFGAEVDTDFGTPTFLASKIG 394	
DB	406	DNVEMIKALIVFGAEVDTDFGTPTFLASKIG 439	

RESULT 2